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OM protein - protein search, using sw model

Run on: January 13, 2006, 11:51:35 ; Search time 76 Seconds
(without alignments)
185.002 Million cell updates/sec

Title: US-10-823-425-6
Perfect score: 157
Sequence: 1 KWLKFKIGAVLVKLVLTGLPALKLTLLK 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003Bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	157	100.0	32	3	AAY87363 Cationic
2	152	96.8	33	3	AAY87366 Cationic
3	142.5	90.8	31	3	AAY87365 Cationic
4	141	89.8	30	3	AAY87364 Cationic
5	132.5	84.4	29	3	AAY87398 Cationic
6	123.5	80.6	1105	9	ADU81674 Antimicro
7	123.5	78.7	28	2	AAY00274 Antimicro
8	123.5	78.7	28	2	AAY14736 Fusion pe
9	123.5	78.7	28	2	AAY40478 Human CEM
10	123.5	78.7	28	2	AAY71688 Cationic
11	123.5	78.7	28	3	AAB12434 CEMA amin
12	123.5	78.7	28	3	AAY91861 Amino aci
13	123.5	78.7	28	3	AAY87358 Cationic
14	123.5	78.7	28	3	AAY87393 Cationic
15	123.5	78.7	28	4	AGG62379 Antimicro
16	123.5	78.7	28	6	ADA00613 Antimicro
17	123.5	78.7	28	7	ADC98982 Synthetic
18	123.5	78.7	34	4	AGG62380 Antimicro
19	123.5	78.7	53	2	AAY71691 R21-R28 p
20	123.5	78.7	124	2	AAY71693 R21-Hpro-
21	123.5	78.7	176	2	AAY71696 R78-hpro-
22	123.5	78.7	178	2	AAY71697 R78-rhpro
23	123.5	78.7	196	2	AAY71694 R21-2Hpro
24	119	75.8	27	5	AAB47908 CEMA. 5/2

ALIGNMENTS

RESULT 1
AAY87363
ID AAY87363 standard; peptide; 32 AA.
XX
AC AAY87363;
XX
DT 03-JUL-2000 (first entry)
XX
DE Cationic antimicrobial peptide, SEQ ID NO:6.
XX
KW Antimicrobial; cationic; antibacterial; antiproliferative; endotoxaemia;
KW sepsis; wound repair; tissue regeneration; transgenic animal;
KW pathogen resistance.
XX
OS Synthetic.
XX
PN WO200012528-A1.
XX
PD 09-MAR-2000.
XX
PF 27-AUG-1999; 99WO-US019646.
XX
PR 28-AUG-1998; 98US-00143124.
XX
(UYBR-) UNIV BRITISH COLUMBIA.
XX
Hancock REW, Gough MA, Patrzykat A, Woods D, Jia X;
XX
WPI; 2000-270790/23.

Novel anti-endotoxemic, antimicrobial peptides useful for inhibiting endotoxaemia/sepsis-associated disorder or cell proliferation, accelerating wound healing, and treating respiratory associated disorder.
Claim 1; Page 93; 116pp; English.
The invention relates to a novel class of cationic antimicrobial peptides (AAY87358-Y87381 and AAY87383-Y87391). It also encompasses nucleotides encoding the peptides and a transgenic animal comprising a nucleotide sequence encoding an anti-microbial peptide. The cationic antimicrobial peptides of the invention are useful for inhibiting the growth of Gram positive or Gram negative bacteria, in combination with an antibiotic or lysozyme. The peptides are also useful for inhibiting the growth of a eukaryotic cell e.g., a neoplastic cell, and sequences AAY87358-Y87369 may be used for inhibiting cell proliferation-associated disorders such as cancer. Peptides AAY87360-Y87369 are useful for inhibiting endotoxaemia or a sepsis-associated disorder such as septic shock. The

CC peptides of the invention may also be used for accelerating wound repair
 CC in a patient when coadministered with a healing agent such as TGF-beta
 CC (transforming growth factor-beta). The peptides are used for treating a
 CC respiratory or pulmonary-associated infection, or a disorder such as
 CC cystic fibrosis. The peptides are used for revitalising scar tissue, for
 CC wound repair in guided tissue degeneration (GTR) procedures, and for
 CC promoting tissue growth in skin grafts. Nucleic acids encoding peptides
 CC AAY87372-Y87378 and AAY87383-Y87391 may be used in the generation of
 CC transgenic animals, with nucleotide encoding sequences AAY87372 and
 CC AAY87374-Y87378 being particularly useful for the generation of
 CC transgenic fish with enhanced resistance to pathogenic organisms.
 CC Sequences AAY87358-Y87381 and AAY87383-Y87391 represent cationic
 CC antimicrobial peptides claimed for use in various embodiments of the
 CC invention
 CC
 XX SQ Sequence 32 AA;

Query Match 100.0%; Score 157; DB 3; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.9e-16;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KWLKKIGIGAVLKVLTGTPALKLT 32
 |||||
 DB 1 KWLKKIGIGAVLKVLTGTPALKLT 32

RESULT 2
 AAY87366
 ID AAY87366 standard; peptide; 33 AA.
 XX
 AC AAY87366;
 XX
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE Cationic antimicrobial peptide, SEQ ID NO:9.
 XX
 KW Antimicrobial; cationic; antibacterial; antiproliferative; endotoxaemia;
 KW sepsis; wound repair; tissue regeneration; transgenic animal;
 KW pathogen resistance.
 XX
 OS Synthetic.
 XX
 PN WO200012528-A1.
 XX
 PD 09-MAR-2000.
 XX
 XX 27-AUG-1999; 99WO-US019646.
 XX
 XX 28-AUG-1998; 98US-00143124.
 XX
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 XX
 XX Hancock REW, Gough MA, Patrzykat A, Woods D, Jia X;
 XX WPI; 2000-270790/23.
 DR
 XX Novel anti-endotoxic, antimicrobial cationic peptides useful for
 PT inhibiting endotoxaemia/sepsis-associated disorder or cell proliferation,
 PT accelerating wound healing, and treating respiratory associated disorder.
 XX
 XX Claim 1; Page 93; 116pp; English.

XX The invention relates to a novel class of cationic antimicrobial peptides
 CC (AAY87358-Y87381 and AAY87383-Y87391). It also encompasses nucleotides
 CC encoding the peptides and a transgenic animal comprising a nucleotide
 CC sequence encoding an anti-microbial peptide. The cationic antimicrobial
 CC peptides of the invention are useful for inhibiting the growth of Gram
 CC positive or Gram negative bacteria, in combination with an antibiotic or
 CC lysosyme. The peptides are also useful for inhibiting the growth of a
 CC eukaryotic cell e.g., a neoplastic cell, and sequences AAY87358-Y87369
 CC may be used for inhibiting cell proliferation-associated disorders such
 CC as cancer. Peptides AAY87360-Y87369 are useful for inhibiting
 CC endotoxaemia or a sepsis-associated disorder such as septic shock. The

CC peptides of the invention may also be used for accelerating wound repair
 CC in a patient when coadministered with a healing agent such as TGF-beta
 CC (transforming growth factor-beta). The peptides are used for treating a
 CC respiratory or pulmonary-associated infection, or a disorder such as
 CC cystic fibrosis. The peptides are used for revitalising scar tissue, for
 CC wound repair in guided tissue degeneration (GTR) procedures, and for
 CC promoting tissue growth in skin grafts. Nucleic acids encoding peptides
 CC AAY87372-Y87378 and AAY87383-Y87391 may be used in the generation of
 CC transgenic animals, with nucleotide encoding sequences AAY87372 and
 CC AAY87374-Y87378 being particularly useful for the generation of
 CC transgenic fish with enhanced resistance to pathogenic organisms.
 CC Sequences AAY87358-Y87381 and AAY87383-Y87391 represent cationic
 CC antimicrobial peptides claimed for use in various embodiments of the
 CC invention
 CC
 XX SQ Sequence 33 AA;

Query Match 96.8%; Score 152; DB 3; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KWLKKIGIGAVLKVLTGTPALKLT 32
 |||||
 DB 3 KWLKKIGIGAVLKVLTGTPALKLT 33

RESULT 3
 AAY87365
 ID AAY87365 standard; peptide; 31 AA.
 XX
 AC AAY87365;
 XX
 XX 03-JUL-2000 (first entry)
 XX
 DE Cationic antimicrobial peptide, SEQ ID NO:8.
 XX
 KW Antimicrobial; cationic; antibacterial; antiproliferative; endotoxaemia;
 KW sepsis; wound repair; tissue regeneration; transgenic animal;
 KW pathogen resistance.
 XX
 OS Synthetic.
 XX
 PN WO200012528-A1.
 XX
 PD 09-MAR-2000.
 XX
 XX 27-AUG-1999; 99WO-US019646.
 XX
 XX 28-AUG-1998; 98US-00143124.
 XX
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 XX
 XX Hancock REW, Gough MA, Patrzykat A, Woods D, Jia X;
 XX WPI; 2000-270790/23.
 DR
 XX Novel anti-endotoxic, antimicrobial cationic peptides useful for
 PT inhibiting endotoxaemia/sepsis-associated disorder or cell proliferation,
 PT accelerating wound healing, and treating respiratory associated disorder.
 XX
 XX Claim 1; Page 93; 116pp; English.

XX The invention relates to a novel class of cationic antimicrobial peptides
 CC (AAY87358-Y87381 and AAY87383-Y87391). It also encompasses nucleotides
 CC encoding the peptides and a transgenic animal comprising a nucleotide
 CC sequence encoding an anti-microbial peptide. The cationic antimicrobial
 CC peptides of the invention are useful for inhibiting the growth of Gram
 CC positive or Gram negative bacteria, in combination with an antibiotic or
 CC lysosyme. The peptides are also useful for inhibiting the growth of a
 CC eukaryotic cell e.g., a neoplastic cell, and sequences AAY87358-Y87369
 CC may be used for inhibiting cell proliferation-associated disorders such
 CC as cancer. Peptides AAY87360-Y87369 are useful for inhibiting
 CC endotoxaemia or a sepsis-associated disorder such as septic shock. The

CC peptides of the invention may also be used for accelerating wound repair
 CC in a patient when coadministered with a healing agent such as TGF-beta
 CC (transforming growth factor-beta). The peptides are used for treating a
 CC respiratory or pulmonary-associated infection, or a disorder such as
 CC cystic fibrosis. The peptides are used for revitalising scar tissue, for
 CC wound repair in guided tissue degeneration (GTR) procedures, and for
 CC promoting tissue growth in skin grafts. Nucleic acids encoding peptides
 CC AAY87372-Y87378 and AAY87383-Y87391 may be used in the generation of
 CC transgenic animals, with nucleotide encoding sequences AAY87372 and
 CC AAY87374-Y87378 being particularly useful for the generation of
 CC transgenic fish with enhanced resistance to pathogenic organisms.
 CC Sequences AAY87382 and AAY87392-Y87401 represent cationic antimicrobial
 CC peptides used in exemplifications of the present invention
 XX
 SQ Sequence 29 AA;

Query Match 84.4%; Score 132.5; DB 3; Length 29;
 Best Local Similarity 90.6%; Pred. No. 9.4e-13;
 Matches 29; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KKKLKKIGIGAVLVKLVLTGTPALKLT 32
 |||||
 Db 1 KKKLKKIGIGAVLVKLVLTGTPALKLT 29

RESULT 6

ADU81674
 ID ADU81674 standard; protein; 1105 AA.

AC ADU81674;

DT 10-FEB-2005 (first entry)

XX Antimicrobial peptide MBI-28/silk-elastin polymer MBI-SELK47K, SEQ ID:33.
 XX Protein engineering; protein stabilization; cosmetics; textile; filter;
 KW fibroin; elastin; fusion protein; antimicrobial-gen. .

XX Bombyx mori.
 OS Vertebrata.
 OS Chimeric.
 OS Synthetic.

XX US2004234609-A1.

XX 25-NOV-2004.

XX 14-MAY-2004; 2004US-00845936.

XX 14-MAY-2003; 2003US-0470464P.

XX (COLL/) COLLIER K D.

PA (CUEV/) CUEVAS W A.

PA (KUMA/) KUMAR M.

XX Collier KD, Cuevas WA, Kumar M;

XX WPI; 2005-046149/05.

XX Biomolecular conjugates useful in personal care products e.g. hair care
 PT composition, cosmetic, oral care composition, comprising conjugation
 PT product of repeat sequence protein polymer and active agents.

XX Claim 30; SEQ ID NO 33; 54pp; English.

XX The invention relates to biomolecular conjugates comprising a repeat
 CC sequence protein polymer (i.e., an engineered protein) and at least one
 CC active agent, such as silicones, fragrances, dyes, tints, UV actives,
 CC sunscreens, lanolin, vitamins, bleaches, thickening agents,
 CC antimicrobials and biologically active polypeptides. The repeat sequence
 CC protein polymer preferably comprises a repeating amino acid sequence unit
 CC derived from elastin, collagen, abductin, byssus, flagelliform silk,
 CC dragline silk, gluten high molecular weight subunit, titin, fibronectin,

CC laminin, gliadin, glue polypeptide, ice nucleating protein, keratin,
 CC mucin, RNA polymerase II, resilin or mixtures thereof. The repeat
 CC sequence protein polymers provide a scaffolding to which active agents
 CC may be bound. In particular, they enhance the ability to utilize proteins
 CC and peptides as active agents as they overcome many of the
 CC hydrophobicity, solubility, and binding limitations associated with
 CC polypeptide active agents, and allow the use of polypeptide active agents
 CC in applications for which a total protein environment is desirable. The
 CC invention also relates to personal care compositions comprising a
 CC biomolecular conjugate of the invention; a method of making the personal
 CC care compositions; a method of making a biomolecular conjugate by
 CC recombinantly producing a fusion protein comprising the repeat sequence
 CC protein polymer and a polypeptide active agent; biomaterials adapted for
 CC at least one predetermined desirable function which comprise one or more
 CC biomolecular conjugates comprising a silk elastin polymer as the repeat
 CC sequence protein polymer and a polypeptide active agent; and a method of
 CC producing such biomaterials. The biomolecular conjugates are useful in
 CC personal care compositions such as over-the counter pharmaceutical
 CC compositions, and compositions used for hair care, skin care, nail care,
 CC oral care and cosmetics. The biomolecular conjugates are also useful in
 CC biomaterials such as textiles (e.g., protective garments), filters,
 CC creams, coatings, and dressings, and in biomaterials useful in genetics
 CC research tools or in search and/or identification tools. The present
 CC sequence represents a specifically claimed biomolecular conjugate
 CC comprising the silk-elastin polymer SELP47K (ADU81661) N-terminally fused
 CC to antimicrobial peptide MBI-28 (ADU81679).

XX SQ Sequence 1105 AA;

Query Match 80.6%; Score 126.5; DB 9; Length 1105;
 Best Local Similarity 87.5%; Pred. No. 4.8e-10;
 Matches 28; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 KKKLKKIGIGAVLVKLVLTGTPALKLT 32
 |||||
 Db 190 KKKLKKIGIGAVLVKLVLTGTPALKLT 218

RESULT 7

AAW00274

ID AAW00274 standard; peptide; 28 AA.

XX AAW00274;

XX 21-MAY-1997 (first entry)

XX Antimicrobial peptide, CEMA.

XX Cationic peptide; CEMA; CEME; cecropia; melittin; bacterial growth;
 KW antibiotic activity; permeable; bacterial outer membrane;
 KW lipopolysaccharide; fusion peptide; inhibition; endotoxaemia;
 KW sepsis associated disorder; septic shock.

XX Synthetic.

XX WO9628559-A1.

XX 19-SEP-1996.

XX 13-MAR-1996; 96WO-IB000431.

XX 13-MAR-1995; 95US-00405234.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Hancock RW, Piers KL, Brown MH, Kelly N;

XX WPI; 1996-433831/43.

XX Recombinant production of antimicrobial, cationic peptide - produced in
 PT bacterial host as fusion peptide with an anionic portion for suppressing
 PT the anti-microbial activity of the cationic peptide.

XX

WPI; 1997-099468/09.

Prod'n. of recombinant cationic peptide with antimicrobial activity - in the form of a fusion peptide with protease-inhibiting anionic peptide.

Example 1; Fig 3; 31pp; English.

The sequences given in AAW14734-36 represent HNP-1, CEME and CEMA respectively. HNP-1 is peptide 1 from human neutrophil protein, CEME is a fusion peptide made from portions of an insect defensin cecropin A and the bee venom peptide melittin, and CEMA is a variant of CEME with two additional lysine residues at the C-terminal end. The modification from CEME to CEMA causes a two-fold improvement in antibiotic activity against many bacterial species as well as substantially enhancing the ability to permeabilise bacterial outer membranes and binding to lipopolysaccharides. CEMA may be used synergistically with classical antibiotics to break down the outer membrane permeability barrier. It is possibly active against *E. coli*, *Pseudomonas aeruginosa*, *E. cloacae*, *S. typhimurium* and *S. aureus*. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 27-AUG-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field)

```
SQ Sequence 28 AA;                                78.7%; Score 123.5; DB 2; Length 28;  
Query Match Best Local Similarity 90.0%; Pred. No. 2.2e-11;  
Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1  
  
QY      1 KWLKFKKGICIGAVLKVLRVLTGTPALKLT 30
```

RESULT 9	
AAW40478	
ID	AAW40478 standard; protein; 28 AA.
XX	
AC	AAW40478;
XX	
DT	14-JUL-1998 (first entry)
XX	
XX	Human CEMA peptide.
XX	
KW	Cecropin A; mellitin; CEME; fusion protein; polycationic; antibacterial;
KW	permeable; outer membrane; lipopolysaccharide; bacterial infection;
KW	septic shock; CEMA.
XX	
OS	Homo sapiens.

XX	US5707855-A.
PN	
XX	
XX	13-JAN-1998.
PD	
XX	
XX	20-DEC-1996; 96US-00770557.
PF	
XX	
XX	21-AUG-1992; 92US-009333492.
PR	20-AUG-1993; 93US-00110502.
PR	20-DEC-1995; 95US-00575052.
XX	

XX
XX
XX
PI Brown MH, Piers KL, Hancock RW;
XX
XX WPI; 1998-100348/09.
XX
XX Antibacterial peptide CEMA - useful for treating bacterial infections and
PT septic shock.
PT
XX
PS Disclosure; Fig 3; 3lpp; English.
XX
XX
CC
CC This sequence is a novel polycationic antibacterial peptide, CEMA. This
CC peptide is a hybrid comprising the first 18 amino acids of cecropin

CC A and the last 8 amino acids of melittin. It has two Lys residues at the
 CC C terminus which creates a sequence with two-fold increased antibiotic
 CC activity against many bacterial species as well as enhanced ability to
 CC permeabilise bacterial outer membranes and bind to lipopolysaccharide.
 CC CEMA can be used to treat bacterial infections and septic shock
 XX
 SQ Sequence 28 AA;

Query Match 78.7%; Score 123.5; DB 2; Length 28;
 Best Local Similarity 90.0%; Pred. No. 2.2e-11;
 Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KWKLFKKIGIGAVLVKLVLTGTPALKLT 30
 DB 1 KWKLFKKIGIGA---VLKVLTTGLPALKLT 27

RESULT 10
 AAW71688
 ID AAW71688 standard; peptide; 28 AA.
 XX
 AC AAW71688;
 XX

DT 11-JAN-1999 (first entry)
 XX

DE Cationic peptide MBI28 (MW 3051).
 XX

KW MBI28; cationic peptide; plasmid pKLI; small cryptic plasmid;
 KW replication; RepA; vector; RAMP.
 XX

OS Synthetic.
 XX

XX WO9841636-A2.
 PN

XX 24-SEP-1998.
 PD

XX 16-MAR-1998; 98WO-CA000214.
 PP

XX 14-MAR-1997; 97US-0040722P.
 PR

XX (BURI/) BURIAN J.
 PA

PA (KAYW/) KAY W W.
 PA

PI Burian J, Kay WW;
 XX

XX WPI; 1998-531571/45.
 XX

XX Increasing plasmid copy number in a cell with the repA gene product - and
 PT an small cryptic plasmid ori sequence, useful for high level expression
 PT of e.g. cytokines, antigens or therapeutic proteins.
 XX

PS Example 13; Page 54; 82pp; English.
 XX

XX MBI28 is a small (mol.wt. 3051) cationic peptide. Plasmids have been
 CC constructed in which MBI28 is fused to a replication leader (R21 or R78)
 CC sequence of RepA (see also AAW71688), a protein involved in regulating
 CC replication of pKLI (see AAV58252), a small cryptic plasmid of
 CC Escherichia coli. Plasmids encoding fusion proteins (see AAW61792-97)
 CC comprising R21 or R78, Hpro (see AAW71692) and MBI28 have been
 CC constructed and utilised in the construction of novel expression vectors.
 CC The invention provides controlled replication plasmid vectors (RAMP
 CC vectors) comprising a replication origin of a small cryptic plasmid and a
 CC gene encoding RepA. The vectors can reach very high levels of plasmid
 CC replication, but are not lethal to the host cell, and can be used to
 CC direct the high level expression of e.g. cytokines, antigens and
 CC therapeutic proteins
 XX

XX Sequence 28 AA;
 SQ

Query Match 78.7%; Score 123.5; DB 2; Length 28;
 Best Local Similarity 90.0%; Pred. No. 2.2e-11;
 Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KWKLFKKIGIGAVLVKLVLTGTPALKLT 30
 DB 1 KWKLFKKIGIGA---VLKVLTTGLPALKLT 27

RESULT 11
 AAB12434
 ID AAB12434 standard; peptide; 28 AA.
 XX
 AC AAB12434;
 XX

DT 20-OCT-2000 (first entry)
 XX

XX CEMA amino acid sequence.
 XX

XX CEMA; Pro-CEMA; dermaseptin B; temporin A; cecropin A; melittin;
 KW CaMA 35S promoter; cationic polypeptide; antimicrobe; transgenic plant;
 KW expression vector; agrobacillus; callus; phytopathogen; bacteria; fungus;
 KW calli; antifungal; antibacterial.
 XX

XX Unidentified.
 OS

XX CN1249310-A.
 PN

XX 05-APR-2000.
 PD

XX 28-SEP-1998; 98CN-00112269.
 PP

XX 28-SEP-1998; 98CN-00112269.
 PR

XX (ZHOU/) ZHOU G.
 PA

XX Zhou G;
 PI

XX WPI; 2000-400710/35.
 DR

XX Cationic polypeptide process for expressing antimicrobe in plant.
 XX

XX Claim 2; Page 1; 7pp; Chinese.
 PS

XX The present invention describes a transgenic plant expression vector
 CC containing three antimicrobe cationic polypeptides. The plant tissue is
 CC introduced to these genes via agrobacillus and in the callus culture, the
 CC callus resisting phytopathogen (bacteria and fungus) can be externally
 CC chosen. Choosing these calli can regenerate plants and directly test its
 CC antifungal and antibacterial powder. After these transgenic plants are
 CC ripened, whole or partial plant can be harvested. The present sequence
 CC represents a specifically claimed peptide from the present invention
 XX Sequence 28 AA;
 SQ

Query Match 78.7%; Score 123.5; DB 3; Length 28;
 Best Local Similarity 90.0%; Pred. No. 2.2e-11;
 Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KWKLFKKIGIGAVLVKLVLTGTPALKLT 30
 DB 1 KWKLFKKIGIGA---VLKVLTTGLPALKLT 27

RESULT 12
 AAY91861
 ID AAY91861 standard; peptide; 28 AA.
 XX
 AC AAY91861;
 XX

DT 06-JUN-2000 (first entry)
 XX

XX Amino acid sequence of cationic peptide MBI 28.
 DE

XX Cationic peptide; tumour; pharmaceutical composition; cancer; treatment;
 KW leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma;
 KW breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;

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OM protein - protein search, using sw model

Run on: January 13, 2006, 11:56:31 ; Search time 23 Seconds
(without alignments)
115.027 Million cell updates/sec

Title: US-10-823-425-6
Perfect score: 157
Sequence: 1 KWLFKKIGIGAVLKVLTGLPALKLTLLK 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/1/1aa/6-COMB.pep.*
3: /cgn2_6/prodata/1/1aa/H-COMB.pep.*
4: /cgn2_6/prodata/1/1aa/PCUTS-COMB.pep.*
5: /cgn2_6/prodata/1/1aa/RE-COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	157	100.0	32	2 US-09-143-124-6	Sequence 6, Appli
2	157	100.0	32	2 US-09-908-139-6	Sequence 6, Appli
3	152	96.8	33	2 US-09-143-124-9	Sequence 9, Appli
4	152	96.8	33	2 US-09-908-139-9	Sequence 9, Appli
5	142.5	90.8	31	2 US-09-143-124-8	Sequence 8, Appli
6	142.5	90.8	31	2 US-09-908-139-8	Sequence 8, Appli
7	141	89.8	30	2 US-09-143-124-7	Sequence 7, Appli
8	141	89.8	30	2 US-09-908-139-7	Sequence 7, Appli
9	123.5	78.7	28	1 US-08-575-052-24	Sequence 24, Appli
10	123.5	78.7	28	1 US-08-614-516A-24	Sequence 24, Appli
11	123.5	78.7	28	1 US-08-770-557-24	Sequence 24, Appli
12	123.5	78.7	28	1 US-08-405-234-24	Sequence 24, Appli
13	123.5	78.7	28	1 US-08-460-464B-15	Sequence 15, Appli
14	123.5	78.7	28	2 US-09-143-124-1	Sequence 1, Appli
15	123.5	78.7	28	2 US-09-042-071-34	Sequence 34, Appli
16	123.5	78.7	28	2 US-09-030-619-121	Sequence 121, App
17	123.5	78.7	28	2 US-09-908-139-1	Sequence 1, Appli
18	123.5	78.7	28	2 US-10-225-087-112	Sequence 112, App
19	123.5	78.7	53	2 US-09-042-071-37	Sequence 37, Appli
20	123.5	78.7	124	2 US-09-042-071-39	Sequence 39, Appli
21	123.5	78.7	178	2 US-09-042-071-42	Sequence 42, Appli
22	123.5	78.7	178	2 US-09-042-071-43	Sequence 43, Appli
23	123.5	78.7	195	2 US-09-042-071-40	Sequence 40, Appli
24	123.5	78.7	195	2 US-09-042-071-41	Sequence 41, Appli
25	117.5	74.8	28	2 US-08-658-857B-37	Sequence 37, Appli
26	117.5	74.8	28	2 US-08-763-226C-37	Sequence 37, Appli
27	117.5	74.8	28	2 US-09-307-200-37	Sequence 37, Appli

28 117.5 74.8 28 2 US-09-593-321-37 Sequence 37, Appli
29 117.5 74.8 28 2 US-10-272-248-37 Sequence 37, Appli
30 110 70.1 30 2 US-09-143-124-11 Sequence 11, Appli
31 110 70.1 30 2 US-09-908-139-11 Sequence 11, Appli
32 109.5 69.7 26 1 US-08-575-052-23 Sequence 23, Appli
33 109.5 69.7 26 1 US-08-614-516A-23 Sequence 23, Appli
34 109.5 69.7 26 1 US-08-770-557-23 Sequence 23, Appli
35 109.5 69.7 26 1 US-08-405-234-23 Sequence 23, Appli
36 109.5 69.7 26 1 US-08-460-464B-14 Sequence 14, Appli
37 109.5 69.7 26 2 US-08-658-857B-36 Sequence 36, Appli
38 109.5 69.7 26 2 US-08-763-226C-36 Sequence 36, Appli
39 109.5 69.7 26 2 US-09-307-200-36 Sequence 36, Appli
40 109.5 69.7 26 2 US-09-593-321-36 Sequence 36, Appli
41 109.5 69.7 26 2 US-09-030-619-120 Sequence 120, App
42 109.5 69.7 26 2 US-10-225-087-111 Sequence 111, App
43 109.5 69.7 26 2 US-09-904-753-13 Sequence 13, Appli
44 109.5 69.7 26 2 US-10-272-248-36 Sequence 36, Appli
45 91.5 58.3 26 2 US-08-658-857B-11 Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-09-143-124-6
; Sequence 6, Application US/09143124
; Patent No. 6288212
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/143,124
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-143-124-6

Query Match 100.0%; Score 157; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KWLFKKIGIGAVLKVLTGLPALKLTLLK 32
DB 1 KWLFKKIGIGAVLKVLTGLPALKLTLLK 32

RESULT 2
US-09-908-139-6
; Sequence 6, Application US/09908139
; Patent No. 6818407
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/908,139
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/143,124


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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide

```


Patent No. 5688767
; GENERAL INFORMATION:
; APPLICANT: HANCOCK, ROBERT E.W.
; APPLICANT: PIERS, KEVIN L.
; APPLICANT: BROWN, MELISSA H.
; APPLICANT: KELLY, NIAMH
; TITLE OF INVENTION: TREATMENT OF ENDOTOXIN-ASSOCIATED
; DISORDERS WITH CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Ste. 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/614,516A
; FILING DATE: 13-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILE, PH.D., LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/010001
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: CEMA
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..28
US-08-614-516A-24

Query Match 78.7%; Score 123.5; DB 1; Length 28;
Best Local Similarity 90.0%; Pred. No. 2.4e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KWKLFKKIGIGAVLKVLTGTPALKLT 30
Db 1 KWKLFKKIGIGA---VLKVLTTGLPALKLT 27

RESULT 11
US-08-770-557-24
; Sequence 24, Application US/08770557
; Patent No. 5707855
; GENERAL INFORMATION:
; APPLICANT: HANCOCK, ROBERT E.W.
; APPLICANT: PIERS, KEVIN L.
; APPLICANT: BROWN, MELISSA H.
; TITLE OF INVENTION: CATIONIC PEPTIDES AND METHOD FOR PRODUCTION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JURAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/770,557
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/575,052
FILING DATE:
APPLICATION NUMBER: US/08/110,502
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR., PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2823
TELEPHONE: 619/455-5100
TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: CEMA
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..28
US-08-770-557-24

Query Match 78.7%; Score 123.5; DB 1; Length 28;
Best Local Similarity 90.0%; Pred. No. 2.4e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KWKLFKKIGIGAVLKVLTGTPALKLT 30
Db 1 KWKLFKKIGIGA---VLKVLTTGLPALKLT 27

RESULT 12
US-08-405-234-24
; Sequence 24, Application US/08405234
; Patent No. 5789377
; GENERAL INFORMATION:
; APPLICANT: HANCOCK, ROBERT E.W.
; APPLICANT: PIERS, KEVIN L.
; APPLICANT: BROWN, MELISSA H.
; APPLICANT: KELLY, NIAMH
; TITLE OF INVENTION: TREATMENT OF ENDOTOXIN-ASSOCIATED DISORDERS
; WITH CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JURAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/405,234
; FILING DATE: 13-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILE, PH.D., LISA A.

REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD3535
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: CEWA
NAME/KEY: Peptide
LOCATION: 1..28
US-08-405-234-24

Query Match 78.7%; Score 123.5; DB 1; Length 28;
Best Local Similarity 90.0%; Pred. No. 2.4e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KWKLFKKIGIGAVLVKLVLTGTPALKLT 30
|||||
DB 1 KWKLFKKIGIGAVLVKLVLTGTPALKLT 27

RESULT 13
US-08-460-464B-15
Sequence 15, Application US/08460464B
Patent No. 5877274
GENERAL INFORMATION:
APPLICANT: Hancock, Robert E.W.
APPLICANT: Karunaratne, Nedra
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,464B
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07420/008001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-464B-15

Query Match 78.7%; Score 123.5; DB 1; Length 28;
Best Local Similarity 90.0%; Pred. No. 2.4e-11;

Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KWKLFKKIGIGAVLVKLVLTGTPALKLT 30
|||||
DB 1 KWKLFKKIGIGAVLVKLVLTGTPALKLT 27

RESULT 14
US-09-143-124-1
Sequence 1, Application US/09143124
Patent No. 6288212
GENERAL INFORMATION:
APPLICANT: Hancock, Robert E. W.
APPLICANT: Gough, Monisha A.
APPLICANT: Patrzykat, Aleksander
APPLICANT: Woods, Donald
APPLICANT: Jia, Xiaoyan
TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
PEPTIDES AND METHODS OF USE THEREFOR
FILE REFERENCE: 07422/016001
CURRENT APPLICATION NUMBER: US/09/143,124
CURRENT FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antimicrobial cationic peptide
US-09-143-124-1

Query Match 78.7%; Score 123.5; DB 2; Length 28;
Best Local Similarity 90.0%; Pred. No. 2.4e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KWKLFKKIGIGAVLVKLVLTGTPALKLT 30
|||||
DB 1 KWKLFKKIGIGAVLVKLVLTGTPALKLT 27

RESULT 15
US-09-042-071-34
Sequence 34, Application US/09042071
Patent No. 6294372
GENERAL INFORMATION:
APPLICANT: Burian, Jan
APPLICANT: Kay, William W.
TITLE OF INVENTION: REPLICATION GENES AND GENE PRODUCTS FROM
SMALL CRYPTIC PLASMIDS AND METHODS FOR CONSTRUCTING
CONTROLLED-REPLICATION PLASMID VECTORS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,071
FILING DATE: 13-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 660081.407
TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-042-071-34

Query Match 78.7%; Score 123.5; DB 2; Length 28;
Best Local Similarity 90.0%; Pred. No. 2.4e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KWKLFPKIGIGAVLVKLVLTGTPALKLT 30
|||
DB 1 KWKLFPKIGIGA--VLKVLTTGLPALKLT 27
|||

Search completed: January 13, 2006, 12:01:25
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2006, 11:53:05 ; Search time 16 Seconds

(without alignments)
192.434 Million cell updates/sec

Title: US-10-823-425-6
Perfect score: 157
Sequence: 1 KWKLFKKIGAVLKVLKLTGTPALKLTLLK 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: Pirl:*
2: Pirl:*
3: Pirl:*
4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64.5	41.1	26	1 MEHBC1	melittin, major -
2	64.5	41.1	27	1 MEH82	melittin, minor -
3	64.5	41.1	70	1 MPH81	melittin, major, p
4	59.5	37.9	26	1 MEH8CD	melittin - giant h
5	54.5	34.7	26	1 MEH8CF	melittin - little
6	53.5	34.1	161	2 C70774	hypothetical prote
7	53	33.8	105	2 E82047	met repressor VC26
8	52	33.1	352	2 S70972	bfpE protein - Esc
9	52	33.1	520	2 B96517	hypothetical prote
10	51	32.5	307	2 S55596	hypothetical prote
11	51	32.5	1091	2 C95133	exonuclease RxB [
12	51	32.5	1091	2 G98001	second chain of ma
13	50	31.8	105	2 AH0014	transcription repr
14	50	31.8	273	2 AC1435	hypothetical prote
15	50	31.8	319	2 T33609	hypothetical prote
16	50	31.8	557	2 T49811	probable vacuolar
17	49.5	31.5	250	2 H83213	hypothetical prote
18	49	31.2	305	2 T29330	hypothetical prote
19	49	31.2	345	2 C72760	probable heme expo
20	49	31.2	749	2 A75560	conserved hypotet
21	49	31.2	779	2 AC2249	heterocyst differe
22	48.5	30.9	616	2 T47679	methionine-tRNA li
23	48	30.6	168	2 C72325	hypothetical prote
24	48	30.6	186	2 E82270	hypothetical prote
25	48	30.6	208	2 A24184	T-cell surface gly
26	48	30.6	213	2 A34953	T-cell surface gly
27	48	30.6	213	2 A30585	T-cell surface gly
28	48	30.6	375	2 B75220	replication factor
29	48	30.6	479	2 B69399	activator 1, repli

30	48	30.6	576	2 S01965	RNA-directed RNA p
31	48	30.6	1235	2 C71210	probable DNA-dirc
32	47.5	30.3	123	2 H75149	hypothetical prote
33	47.5	30.3	246	2 D70143	hypothetical prote
34	47.5	30.3	553	2 T48486	hypothetical prote
35	47.5	30.3	616	2 T50641	methionine-tRNA li
36	47.5	30.3	934	2 H88391	protein R06B10.2 [
37	47.5	30.3	1405	1 S13421	polymERIC globin a
38	47	29.9	283	2 S76994	hypothetical prote
39	47	29.9	287	2 E75159	hypothetical prote
40	47	29.9	317	2 B98208	probable uspA prot
41	47	29.9	317	2 AG3078	hypothetical prote
42	47	29.9	371	2 D90192	alcohol dehydrogen
43	47	29.9	437	2 T47831	hypothetical prote
44	47	29.9	926	2 S36742	cation-transprotin
45	47	29.9	1541	2 S46686	hypothetical prote

ALIGNMENTS

RESULT 1

MEHBC1
melittin, major - Indian honeybee
C;Species: Apis mellifera cerana (Indian honeybee)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
C;Accession: A01762
R;Kreil, G.
PEBS Lett. 33, 241-244, 1973
A;Title: Structure of melittin isolated from two species of honey bees.
A;Reference number: A91392
A;Accession: A01762
A;Molecule type: protein
A;Residues: 1-26 <KRE>

A;Cross-references: UNIPROT:Q8LW54; UNIPARC:UPI000002D010
A;Note: the Indian bee sequence is identical with that of honeybee (Apis mellifera) act
C;Superfamily: melittin
C;Keywords: amidated carboxyl end; hemolysis; homotetramer; venom
F;26/Modified site: amidated carboxyl end (Gln) #status experimental

Query Match 41.1%; Score 64.5; DB 1; Length 26;
Best Local Similarity 84.2%; Pred. No. 0.015;
Matches 16; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 9 GIGAVLKVLKLTGTPAL 27
||| |||||
Db 1 GIGAVLKVLKLTGTPAL 16

RESULT 2

MEH82
melittin, minor - honeybee
C;Species: Apis mellifera (honeybee)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 15-Mar-2004
C;Accession: A01764
R;Habermann, E.; Jentsch, J.
Hoppe-Seyler's Z. Physiol. Chem. 348, 37-50, 1967
A;Title: Sequenzanalyse des Melittins aus den tryptischen und peptischen Spaltstuecken.
A;Reference number: A91640; PMID:68327913; PMID:5592400
A;Accession: A01764
A;Molecule type: protein
A;Residues: 1-27 <HAB>
R;Schroeder, E.; Luebke, K.; Lehmann, M.; Beetz, I.
Experientia 27, 764-765, 1971
A;Title: Haemolytic activity and action on the surface tension of aqueous solutions of
A;Reference number: A91266; PMID:72098668; PMID:5139482
A;Contents: annotation; synthesis
A;Note: the structure was confirmed by synthesis of a peptide with full hemolytic activ
C;Superfamily: melittin
C;Keywords: amidated carboxyl end; hemolysis; homotetramer; venom
F;27/Modified site: amidated carboxyl end (Gln) #status experimental

Query Match 41.1%; Score 64.5; DB 1; Length 27;
 Best Local Similarity 84.2%; Pred. No. 0.015; 0; Mismatches 3; Gaps 1;
 Matches 16; Conservative 0

QY 9 GIGAVLKVLKVLTTGLPAL 27
 ||||| ||||| ||||| ||||| |||||
 Db 1 GIGA---VLKVLTTGLPAL 16

RESULT 3
 MPEB1
 melittin, major precursor [validated] - honeybee
 N:Contains: melittin F
 C:Species: Apis mellifera (honeybee)
 C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
 C:Accession: A91133; A91640; B61285; S23131; A01761; A18880
 R:Vlasak, R.; Unger-Ullmann, C.; Kreil, G.; Frischauf, A.M.
 Eur. J. Biochem. 135, 123-126, 1983
 A>Title: Nucleotide sequence of cloned cDNA coding for honeybee prepromelittin.
 A:Reference number: A91133; MUID:83287387; PMID:6309516
 A:Accession: A91133
 A:Molecule type: mRNA
 A:Residues: 1-70 <VLA>
 A:Cross-references: UNIPROT:P01501; UNIPARC:UPI000012EED4; GB:X02007; NID:95621; PIDN:CA
 R:Habermann, E.; Jentsch, J.
 Hoppe-Seyler's Z. Physiol. Chem. 348, 37-50, 1967
 A>Title: Sequenzanalyse des Melittins aus den tryptischen und peptischen Spaltstuecken.
 A:Reference number: A91640; MUID:68327913; PMID:5592400
 A:Accession: A91640
 A:Molecule type: protein
 A:Residues: 44-69 <HAB>
 A:Cross-references: UNIPARC:UPI000002D010
 R:Gauldie, J.; Hanson, J.M.; Shipoloni, R.A.; Vernon, C.A.
 Eur. J. Biochem. 83, 405-410, 1978
 A>Title: The structures of some peptides from bee venom.
 A:Reference number: A91253; MUID:78126868; PMID:631126
 A:Accession: B61285
 A:Molecule type: protein
 A:Residues: 51-69 <GAU>
 A:Cross-references: UNIPARC:UPI0000173601
 R:Ramalingam, K.; Bello, J.
 Biochem. J. 284, 663-665, 1992
 A>Title: Effect of permethylation on the haemolytic activity of melittin.
 A:Reference number: S23131; MUID:92321983; PMID:1622387
 A:Accession: S23131
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 44-69 <RAM>
 A:Cross-references: UNIPARC:UPI000002D010
 R:Schoeder, E.; Luebke, K.; Lehmann, M.; Beetz, I.
 Experientia 27, 764-765, 1971
 A>Title: Haemolytic activity and action on the surface tension of aqueous solutions of a
 A:Reference number: A91266; MUID:72098668; PMID:5139482
 A:Contents: annotation; synthesis
 A>Note: the structure of melittin was confirmed by synthesis of a peptide with full hem
 R:Kreil, G.; Kreil-Kiss, G.
 Biochem. Biophys. Res. Commun. 27, 275-280, 1967
 A>Title: The isolation of N-formylglycine from a polypeptide present in bee venom.
 A:Reference number: A90165; MUID:67248282; PMID:6040373
 A:Contents: annotation
 A>Note: about 10% of melittin is formylated at the amino end
 R:Luebke, K.; Matthes, S.; Kloes, G.
 Experientia 27, 765-767, 1971
 A>Title: Isolation and structure of N(alpha)-formyl melittin.
 A:Reference number: A91267; MUID:72098669; PMID:5139483
 A:Contents: annotation; synthesis
 A>Note: N-formyl-melittin major was isolated from the venom and its structure was confir
 R:Mollay, C.; Vilas, U.; Kreil, G.
 Proc. Natl. Acad. Sci. U.S.A. 79, 2260-2263, 1982
 A>Title: Cleavage of honeybee prepromelittin by an endoprotease from rat liver microsomes
 A:Reference number: A18880; MUID:82247982; PMID:7048315
 A:Contents: annotation; intact signal sequence after cleavage by partially purified sign
 R:Eisenberg, D.; Gribakov, M.; Terwilliger, T.C.

submitted to the Brookhaven Protein Data Bank, October 1990
 A:Reference number: A50496; PDB:2MLT
 A:Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 44-69
 R:Terwilliger, T.C.; Eisenberg, D.
 J. Biol. Chem. 257, 6010-6015, 1982
 A>Title: The structure of melittin. I. Structure determination and partial refinement.
 A:Reference number: A30639; MUID:82189958; PMID:7076661
 A:Contents: annotation; X-ray crystallography, 2.0 angstroms
 R:Terwilliger, T.C.; Eisenberg, D.
 J. Biol. Chem. 257, 6016-6022, 1982
 A>Title: The structure of melittin. II. Interpretation of the structure.
 A:Reference number: A30640; MUID:82189959; PMID:7076662
 A:Contents: annotation; X-ray crystallography, 2.0 angstroms
 C:Superfamily: melittin
 C:Keywords: amidated carboxyl end; blocked amino end; hemolysis; homotetramer; venom
 F1-21/Domain: signal sequence #status experimental <SIG>
 F122-43/Domain: propeptide #status experimental <PRO>
 F144-69/Product: melittin major #status experimental <MAJ>
 F151-69/Product: melittin F #status experimental <MELF>
 F144/Modified site: formylated amino end (Gly) (in mature form) (partial) #status experi
 F169/Modified site: amidated carboxyl end (Gln) (amide in mature form from following gly

Query Match 41.1%; Score 64.5; DB 1; Length 70;
 Best Local Similarity 84.2%; Pred. No. 0.041;
 Matches 16; Conservative 0; Mismatches 3; Gaps 1;

QY 9 GIGAVLKVLKVLTTGLPAL 27
 ||||| ||||| ||||| ||||| |||||
 Db 44 GIGA---VLKVLTTGLPAL 59

RESULT 4
 MEHBCD
 melittin - giant honeybee (tentative sequence)
 C:Species: Apis mellifera dorsata (giant honeybee)
 C>Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 09-Jul-2004
 C:Accession: A01763
 R:Kreil, G. 54, 100-102, 1975
 FEBS Lett. 175
 A>Title: The structure of Apis dorsata melittin: phylogenetic relationships between hon
 A:Reference number: A01763; MUID:75168194; PMID:1093875
 A:Accession: A01763
 A:Molecule type: protein
 A:Residues: 1-26 <KRE>
 A:Cross-references: UNIPROT:P01502; UNIPARC:UPI000012EED2
 C:Keywords: amidated carboxyl end; homotetramer
 F126/Modified site: amidated carboxyl end (Glu) #status experimental

Query Match 37.9%; Score 59.5; DB 1; Length 26;
 Best Local Similarity 73.7%; Pred. No. 0.076; 0; Indels 3; Gaps 1;
 Matches 14; Conservative 2; Mismatches 0

QY 9 GIGAVLKVLKVLTTGLPAL 27
 ||||| :|||:|||||
 Db 1 GIGA---ILKVLSTGLPAL 16

RESULT 5
 MEHBCF
 melittin - little honeybee
 C:Species: Apis mellifera florea (little honeybee)
 C>Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 09-Jul-2004
 C:Accession: A01765
 R:Kreil, G.
 FEBS Lett. 33, 241-244, 1973
 A>Title: Structure of melittin isolated from two species of honey bees.
 A:Reference number: A91392
 A:Accession: A01765
 A:Molecule type: protein
 A:Residues: 1-26 <KRE>
 A:Cross-references: UNIPROT:P01504; UNIPARC:UPI000012EED3
 C:Superfamily: melittin

C:Keywords: amidated carboxyl end; hemolysis; homotetramer; venom
P:26/Modified site: amidated carboxyl end (Gln) #status experimental

Query Match 34.7%; Score 54.5; DB 1; Length 26;
Best Local Similarity 68.4%; Pred. No. 0.39;
Matches 13; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 9 GIGAVLVKLVLTGTPAL 27
DB 1 GIGA---ILKVLATGLPTL 16

RESULT 6

C70774 hypothetical protein Rv1303 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 05-Oct-2004
C:Accession: C70774
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: C70774

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-161 <COL>

A:Cross-references: UNIPROT:Q10619; UNIPARC:UPI0000031862; GB:273419; GB:AL123456; NID:9

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: Rv1303

C:Superfamily: uncharacterized conserved protein

Query Match 34.1%; Score 53.5; DB 2; Length 161;

Best Local Similarity 43.3%; Pred. No. 3.6;

Matches 13; Conservative 4; Mismatches 8; Indels 5; Gaps 1;

QY 4 LFKKIGIGAV-----LKVLTGTPALK 28

DB 102 IFRPAGLVVFGVLAPFQVLLVATLPLK 131

RESULT 7

E82047

met repressor VC2682 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004

C:Accession: E82047

R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B. I.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: E82047

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <HE1>

A:Cross-references: UNIPROT:Q9KNP9; UNIPARC:UPI00000C337B; GB:AE004333; GB:AE003852; NID

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC2682

A:Map position: 1

C:Superfamily: Met repressor

Query Match 33.8%; Score 53; DB 2; Length 105;

Best Local Similarity 61.9%; Pred. No. 2.7;

Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 KWLFFKIGIGAVLVKLVLT 21

DB 1 KWLFFKIGIGAVLVKLVLT 21

DB 18 KSELYVKITVSIPLKVLKVL 38

RESULT 8

S70972

bfpG protein - Escherichia coli

C:Species: Escherichia coli

C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004

C:Accession: S70972

R:Stone, K.D.; Zhang, H.Z.; Carlson, L.K.; Donnenberg, M.S.

Mol. Microbiol. 20, 325-337, 1996

A:Title: A cluster of fourteen genes from enteropathogenic Escherichia coli is sufficient

A:Reference number: S70966; MUID:96310370; PMID:8733231

A:Accession: S70972

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-352 <STO>

A:Cross-references: UNIPROT:Q47071; UNIPARC:UPI00000B0425; EMBL:Z68186; NID:91122399; P:

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995

C:Genetics:

A:Gene: bfpG

Query Match 33.1%; Score 52; DB 2; Length 352;

Best Local Similarity 31.4%; Pred. No. 13;

Matches 11; Conservative 10; Mismatches 10; Indels 4; Gaps 2;

QY 2 WKLFKK-IGIGAVLVKLVLTGTP---ALKLT 32

DB 207 WSIYTIIGCGLLSLASLINAGIPVPEALRIIMK 241

RESULT 9

B96517

hypothetical protein F16N3.8 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: B96517

R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huijzer, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maity, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96517

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-520 <STO>

A:Cross-references: UNIPROT:Q9SX95; UNIPARC:UPI000009D76D; GB:AE005173; NID:95668797; P:

C:Genetics:

A:Gene: F16N3.8

A:Map position: 1

C:Superfamily: Candida cytochrome P450 52A3; cytochrome P450 homology

Query Match 33.1%; Score 52; DB 2; Length 520;

Best Local Similarity 57.1%; Pred. No. 20;

Matches 12; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 WKLFKKIGIGAVLVKLVLT 22

DB 235 WKLFKKIGIGAVLVKLVLT 255

RESULT 10

S55596

hypothetical protein E2 - equine herpesvirus 2

C:Species: equine herpesvirus 2

C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: S55596

R; Telford, E.A.R.; Watson, M.S.: Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A; Title: The DNA sequence of equine herpesvirus 2.
A; Reference number: S55594; MUID:95302501; PMID:7783207
A; Accession: S55596
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-307 <TEL>
A; Cross-references: UNIPROT:Q66607; UNIPARC:UIP00000F5951; GB:U20824; NID:g6951172; PID#:20824
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995

```
Query Match          32.5%; Score 51; DB 2; Length 307;
Best Local Similarity 44.4%; Pred. No. 16;
Matches 12: Conservative 4; Mismatches 11; Indels 0; Gaps 0;
```

QY 4 LFKKIGIGAVLKVLKVLTTGLPALCLT 30
||||| : || | : | : | : | :
DB 204 LFKKVGEGAYOAVSTISTSSLTTLPLS 239

RESULT 11
C95133
exonuclease RxB [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: C95133
R:Jettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a Virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: C95133
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1091 <KUR>
A:Cross-references: UNIPROT:Q97QQO; UNIPROT:Q8DPR7; UNIPARC:UPI000000C9CC1; GB:AE005672;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI151

Query Match 32.5%; Score 51; DB 2; Length 1091;
Best Local Similarity 50.0%; Pred. No. 58;
Matches 14: Conservative 4; Mismatches 8: Indels 2: Gaps 1;

QY 1 KWKLFKKIGIGAVLKVLTGTLTGLPALK 28
 |||:|||||:|||||:::
Db 468 KWSVFLK--EGAVTKOLODLTTTLEAVE 49

RESULT 12
G98001
second chain of major exonuclease [imported] - Streptococcus pneumoniae (strain R6)
C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_imported 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: G98001
R.; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; F
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; PMID:21429245; PMID:11544234

A;Accession: G98001
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1091 <KUR>
A;Cross-references: UNIP
C;Genetics:

Query Match 32.5%: Score 51: DB 2: Length 1091;

Best Local Similarity 50.0%; Pred. No. 58;
Matches 14; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

```
QY 1 KWLFPKIGIGAVLKVLTITGLPALK 28
   ||| : ||| : ||| : ||| : ||| :
nb 468 KNSVFLK--EGAVTKCOLITLTTRAVE 493
```

RESULT 13
AH0014
transcription repressor protein metJ [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 12-Jul-2004
C/Accession: AH0014
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tithball, R.W.; Holden, M.T.G.; Prentice,
deno-Tarraga, A.M.; Chillingworth, I.; Cronin, A.; Davies, R.M.; Davis, P.; Dou
il, M.; Rutherford, K.; Simmonds, K.; Skelton, J.; Stevens, K.; Whitehead, S.;
Nature 413, 523-527, 2001
A./Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A./Reference number: AB0001: MIUD:21470413: PMID:11586360

A:Accession: AH0014
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-105 <KUR>
 A:Cross-references: UNIPROT;
 C:Genetics:
 A:Gene: metJ
 C:Superfamily: Met repressor

Query Match	31.8%	Score 50;	DB 2;	Length 105;
Best Local Similarity	57.1%;	Pred. No. 7.2;		
Matches 12;	Conservative	2;	Mismatches	7;
				Indels 0;
				Gaps 0;

QY 1 KWKLFKKIGIGAVLKVLT 21
| | | | : | | | : | |
pb 18 KSKOVKKITVSIPLVKLT 38

RESULT 14
AC1435
hypothetical protein lin0018 [imported] - *Listeria innocua* (strain Clip11262)
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AC1435
F:Glaser, F.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kraft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournan,
O. C.; Schlutet, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.;
A:Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1435
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-273 <GLA>
A:Cross-references: UNIPROT:Q92FT5; UNIPARC:UP100000CCOBD; GB:AL592022; PIDN:CA
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin0018

Query Match 31.8%; Score 50; DB 2; Length 273;
Best Local Similarity 45.2%;
Pred. No. 19;
Matches 14; Conservative 11; Indels 4; Gaps 1;
2; Mismatches 11;

Qy 1 KWKLKKIGIGAVLKVLKVLTTGIPALKLT 31
||| : ||| ||| ||| :
Db 10 KWILV----IGLVLVSVFVATTGOAAKETV 36

RESULT 15
T33609
hypoetherical protein F54D10.4 - *Caenorhabditis elegans*

Query Match 31.8%; Score 50; DB 2; Length 319;
Best Local Similarity 37.0%; Pred. No. 23;
Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Search completed: January 13, 2006, 11:59:39
Job time : 17 secs

59

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2006, 11:50:35 ; Search time 71 Seconds
(without alignments)
317.985 Million cell updates/sec

Title: US-10-823-425-6
Perfect score: 157
Sequence: 1 KWKLFKKIGAVLKVLTGLPALKLTLK 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_tmbl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66.5	42.4	67	2 Q95Z19_POLSY	Q95Z19 polistes ap
2	64.5	41.1	70	1 MEL_APICC	P68407 apis cerana
3	64.5	41.1	70	1 MEL_APIME	P01501 apis mellif
4	64.5	41.1	70	1 MEL_VESMC	P59262 vespula mac
5	64.5	41.1	70	1 MEL_VESMG	P68408 vespa magni
6	64.5	41.1	70	1 MEL_VESVN	P68409 vespa velut
7	64.5	41.1	77	1 MEL_APICE	Q81W54 apis cerana
8	59.5	37.9	26	1 MEL_APIDO	P59261 polistes he
9	59.5	37.9	70	1 MEL_POLHE	Q7W49 bordetella
10	59.5	37.9	445	2 Q7W49_BORBR	Q7W281 bordetella
11	59.5	37.9	445	2 Q7W281_BORPA	Q6W11 arthroderna
12	59	37.6	643	2 Q6W11_ARTBE	Q8N1J4 trichophyto
13	56	35.7	643	2 Q8N1J4_TRIRU	Q8GME1 streptomyc
14	56	35.7	1939	2 Q8GME1_STRGL	Q84HN8 streptomyc
15	56	35.7	1956	2 Q84HN8_9ACTO	Q73GG3 treponema d
16	55.5	35.4	478	2 Q73GG3_TREDE	Q7YJU7 calycanthus
17	55	35.0	167	2 Q7YJU7_CALFE	Q61E66 caenorhabdi
18	55	35.0	305	2 Q61E66_CABER	Q8DGC1 synchococc
19	55	35.0	574	2 Q8DGC1_SYNEL	P01504 apis florea
20	54.5	34.7	26	1 MEL_APIFL	Q4T193 tetraodon n
21	54.5	34.7	1206	2 Q4T193_TETNG	Q511C3 entamoeba h
22	54	34.4	340	2 Q511C3_ENTHI	Q50Z36 entamoeba h
23	54	34.4	435	2 Q50Z36_ENTHI	Q511C7 entamoeba h
24	54	34.4	435	2 Q511C7_ENTHI	Q5CR88 cryptospori
25	54	34.4	1567	2 Q5CR88_CRYPV	P64801 mycobacteri
26	53.5	34.1	161	1 Y1303_MYCTO	P64802 mycobacteri
27	53.5	34.1	161	1 Y1335_MYCBO	Q828Z6 streptomyc
28	53.5	34.1	249	2 Q828Z6_STRAM	Q5KY19 geobacillus
29	53.5	34.1	260	2 Q5KY19_GEOKA	Q9KNP9 vibrio chol
30	53	33.8	105	1 METU_VIBCH	Q65147 african swi
31	52.5	33.4	205	2 Q65147_ASP	

32	52.5	33.4	364	2 Q61QP7_CABER	Q61QP7 caenorhabdi
33	52.5	33.4	398	2 Q59MY9_CANAL	Q59MY9 candida alb
34	52.5	33.4	1414	2 Q5TCY1_HUMAN	Q5TCY1 homo sapien
35	52	33.1	352	2 Q47071_ECOLI	Q47071 escherichia
36	52	33.1	363	2 Q4J6Z3_SULAC	Q4J6Z3 sulfolobus
37	52	33.1	509	2 Q64SV1_BACFR	Q64SV1 bacteroides
38	52	33.1	520	2 Q9SX95_ARATH	Q9SX95 arabidopsis
39	51.5	32.8	233	2 Q64CU4_9ARCH	Q64CU4 uncultured
40	51.5	32.8	545	2 Q6N594_RHOPA	Q6N594 rhodospseudo
41	51.5	32.8	811	2 Q4T7L8_TETNG	Q4T7L8 tetraodon n
42	51.5	32.8	1123	2 Q8EWD4_MYCPE	Q8EWD4 mycoplasma
43	51	32.5	142	2 Q4SNCL_TETNG	Q4SNCL tetraodon n
44	51	32.5	216	2 Q8KKH5_CORDI	Q8KKH5 corynebacte
45	51	32.5	307	2 Q66607_9GAWA	Q66607 equid herpe

ALIGNMENTS

RESULT 1

Q95Z19_POLSY Q95Z19_POLSY PRELIMINARY; PRT; 67 AA.

AC Q95Z19;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Melittin.

GN Name=melt;

OS Polistes sp. (Golden paper wasp).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;

OC Vespidae; Polistinae; Polistes.

OX NCBI_TaxID=30210;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Le H.Q.;

RL Thesis (2001), Department of Lab. Molecular Microbiology, Institute of

RL Biotechnology, Hanoi, Viet Nam.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Le H.Q., Nguyen H.M., Le B.T.;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ314920; CAC42164.1; -; Genomic_DNA.

DR HSSP; P01501; 1BHI.

DR GO; GO:0005576; C:extracellular region; IEA.

DR GO; GO:0004860; P:protein kinase inhibitor activity; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR002116; Melittin.

DR Pfam; PF01372; Melittin; I.

FT CHAIN 41 67 melittin.

SQ SEQUENCE 67 AA; 7502 MW; 94821CFF0E4EE9CF CRC64;

Query Match 42.4%; Score 66.5; DB 2; Length 67;

Best Local Similarity 80.0%; Pred. No. 0.16; Mismatches 0; Indels 3; Gaps 1;

Matches 16; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

QY 8 IGIGAVLKVLTGLPAL 27

DB 40 LGIGA---VLKVLTTGLPAL 56

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OC Apidae; Apis.
 OX NCBI_TaxID=94128;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
 RC Li J.-H., Zhang C.-X.;
 RA "Transcription and expression of melittin gene in the venom gland of
 RT the Chinese honeybee, Apis cerana";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Main toxin of bee venom with strong hemolytic activity.
 CC Integrates into cell membranes and has multiple effects, probably,
 CC as a result of its interaction with negatively charged
 CC phospholipids. It inhibits well known transport pumps such as the
 CC Na(+)-K(+)-ATPase and the H(+)-K(+)-ATPase. Increases the
 CC permeability of cell membranes to ions, particularly Na(+) and
 CC indirectly Ca(2+), because of the Na(+)-Ca(2+)-exchange (By
 CC similarity).
 CC -1- SUBUNIT: Monomer and homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: Belongs to the melittin family.
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; AF487907; AAC12201.2; -; mRNA.
 CC EMBL; AJ786346; CAH05131.1; -; Genomic DNA.
 CC HSSP; P01501; 1BH1.
 CC InterPro; IPR002116; Melittin.
 CC Pfam; PF01372; Melittin; 1.
 CC Amidation; Cytolysis; Hemolysis; Signal; Toxin.
 KW SIGNAL 1 21 By similarity.
 FT PROPEP 22 43 Removed by a dipeptidylpeptidase (By
 FT similarity).
 FT PEPTIDE 44 69 Glutamine amide (G-70 provides amide
 FT MOD_RES 69 69 group) (By similarity).
 FT CONFLICT 61 61 G -> S (in Ref. 1; CAH05131).
 FT SEQUENCE 70 AA; 7513 MW; DA7A53C086C9560C CRC64;
 Query Match 41.1%; Score 64.5; DB 1; Length 70;
 Best Local Similarity 84.2%; Pred. No. 0.32;
 Matches 16; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 QY 9 GIGAVLKVLKVLTTGLPAL 27
 Db 44 GIGA---VLKVLTTGLPAL 59
 RESULT 3
 MEL_APIME STANDARD; PRT; 70 AA.
 AC P01501; P01503;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Melittin precursor (Allergen Api m 3) (Api m III).
 GN Names=MELI;
 OS Apis mellifera (Honeybee).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 OC Apidae; Apis.
 OX NCBI_TaxID=7460;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=83287387; PubMed=6309516;
 RA Vlasak R., Unger-Ullmann C., Kreil G., Frischauf A.-M.;
 RT "Nucleotide sequence of cloned cDNA coding for honeybee
 RT prepromelittin";
 RL Eur. J. Biochem. 135:123-126 (1983).
 RN [2]
 RP PROTEIN SEQUENCE OF 44-69 (MELITTIN 1 AND 2).
 RX MEDLINE=6827913; PubMed=5592400;
 RA Habermann E., Jentsch J.;
 RT "Sequence analysis of melittin from tryptic and peptic degradation
 RT products";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:37-50 (1967).
 RN [3]
 RP SYNTHESIS OF 44-69.
 RX MEDLINE=72098668; PubMed=5139482;
 RA Schroeder E., Luebke K., Lehmann M., Beetz I.;
 RT "Hemolytic activity and action on the surface tension of aqueous
 RT solutions of synthetic melittins and their derivatives.";
 RL Experientia 27:764-765 (1971).
 RN [4]
 RP SYNTHESIS OF 44-69.
 RX MEDLINE=72098669; PubMed=5139483;
 RA Luebke K., Matthes S., Kloss G.;
 RT "Isolation and structure of N 1-formyl melittin.";
 RL Experientia 27:765-767 (1971).
 RN [5]
 RP LETHAL CONCENTRATION.
 RX MEDLINE=20132498; PubMed=10669014; DOI=10.1016/S0041-0101(99)00136-1;
 RA Shiomi K., Igarashi T., Yokota H., Nagashima Y., Ishida M.;
 RT "Isolation and structures of graministins, peptide toxins from the skin
 RT secretion of the soapfish Grammistes sexlineatus.";
 RL Toxicon 38:91-103 (2000).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 44-69.
 RX MEDLINE=82189959; PubMed=7076662;
 RA Terwilliger T.C., Eisenberg D.;
 RT "The structure of melittin. II. Interpretation of the structure.";
 RL J. Biol. Chem. 257:6016-6022 (1982).
 RN [7]
 RP STRUCTURE BY NMR OF 44-69.
 RA Barnham K.J., Hewish D., Werkmeister J., Curtain C., Kirkpatrick A.,
 RA Bartome N., Norton R., Rivett D.;
 RL Submitted (JUN-1998) to the PDB data bank.
 RN [8]
 RP REVIEW.
 RX MEDLINE=90254148; PubMed=2187536; DOI=10.1016/0304-4157(90)90006-X;
 RA Dempsey C.E.;
 RT "The actions of melittin on membranes.";
 RL Biochim. Biophys. Acta 1031:143-161 (1990).
 CC -1- FUNCTION: Main toxin of bee venom with strong hemolytic activity.
 CC Integrates into cell membranes and has multiple effects, probably,
 CC as a result of its interaction with negatively charged
 CC phospholipids. It inhibits well known transport pumps such as the
 CC Na(+)-K(+)-ATPase and the H(+)-K(+)-ATPase. Increases the
 CC permeability of cell membranes to ions, particularly Na+ and
 CC indirectly Ca(2+), because of the Na(+)-Ca(2+)-exchange.
 CC -1- SUBUNIT: Monomer and homotrimer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- ALLERGEN: Causes an allergic reaction in human.
 CC -1- TOXIC DOSE: LC(50) is 2.7 ug/ml against killifish.
 CC -1- MISCELLANEOUS: N-formyl-melittin major has 80% of the activity of
 CC melittin.
 CC -1- SIMILARITY: Belongs to the melittin family.
 CC -1- DATABASE: NAME=Protein Spot; NOTE=Issue 12 of July 2001;
 CC WWW="http://www.expasy.org/spotlight/back issues/sptlt012.shtml".
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; X02007; CAA26038.1; -; mRNA.
 CC PIR; A91133; MPBH1.
 CC PDB; 1BH1; NMR; @=44-69.
 CC PDB; 2MLT; X-ray; A/B=44-69.
 CC Ensembl; ENSAPMG0000009127; Apis mellifera.
 DR

DR InterPro: IPR002116; Melittin.
 DR Pfam: PF01372; Melittin; 1.
 DR ProDom: PD014636; Melittin; 1.
 KW 3D-structure; Allergen; Amidation; Cytolysis; Signal; Toxin.
 Direct protein sequencing; Formylation; Hemolysis; Signal; Toxin.
 FT SIGNAL 1 21
 FT PROPEP 22 43 Removed by a dipeptidylpeptidase.
 FT PEPTIDE 44 69 Melittin.
 FT MOD_RES 44 69 N-formylglycine (partial).
 FT MOD_RES 69 69 Glutamine amide (G-70 provides amide group).
 FT VARIANT 64 64 K -> S (in melittin 2; possibly an artifact).
 FT VARIANT 67 70 RQQG -> KRQQ (in melittin 2; possibly an artifact).
 FT HELIX 45 53
 FT TURN 54 54
 FT HELIX 55 68
 FT SEQUENCE 70 AA; 7585 MW; 607F52C091C23BB6 CRC64;
 SQ
 Query Match 41.1%; Score 64.5; DB 1; Length 70;
 Best Local Similarity 84.2%; Pred. No. 0.32;
 Matches 16; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 QY 9 GIGAVLKVLKVLTTGLPAL 27
 Db 44 GIGA---VLKVLTTGLPAL 59

RESULT 4
 MEL_VESMG
 ID MEL_VESMG STANDARD; PRT; 70 AA.
 AC P59262;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Melittin precursor.
 GN Name=MELT;
 OS Vespa maculifrons (Eastern yellow jacket) (Wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespula.
 OX NCBI_TaxID=7453;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC Tissue=Venom gland;
 RX PubMed=12939801;
 RA Shi W.J., Zhang S.F., Zhang C.-X., Cheng J.A.;
 RT Cloning and comparative analysis of the venom prepro-melittin genes
 from four wasp species.";
 RL Yi Chuan Xue Bao 30:555-559(2003).
 CC -1- FUNCTION: Has strong hemolytic activity. Integrates into cell
 membranes and has multiple effects, probably, as a result of its
 interaction with negatively charged phospholipids. It inhibits
 well known transport pumps such as the Na(+)-K(+)-ATPase and the
 H(+)-K(+)-ATPase. Increases the permeability of cell membranes to
 ions, particularly Na+ and indirectly Ca(2+), because of the
 Na(+)-Ca(2+)-exchange (By similarity).
 CC -1- SUBUNIT: Monomer and homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: Belongs to the melittin family.
 CC
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 use as long as its content is in no way modified and this statement is not
 removed.
 CC
 CC EMBL: AF487911; AAO12205.1; -; mRNA.
 CC HSP: P01501; 1BH1.
 CC InterPro: IPR002116; Melittin.
 CC Pfam: PF01372; Melittin; 1.
 CC ProDom: PD014636; Melittin; 1.
 KW Amidation; Cytolysis; Hemolysis; Signal; Toxin.
 FT SIGNAL 1 21
 FT PROPEP 22 43 Removed by a dipeptidylpeptidase (By
 similarity).
 FT PEPTIDE 44 69 Melittin.
 FT MOD_RES 69 69 Glutamine amide (G-70 provides amide
 group) (By similarity).
 FT SEQUENCE 70 AA; 7543 MW;
 SQ

DR ProDom: PD014636; Melittin; 1.
 KW Amidation; Cytolysis; Hemolysis; Signal; Toxin.
 FT SIGNAL 1 21
 FT PROPEP 22 43 Removed by a dipeptidylpeptidase (By
 similarity).
 FT PEPTIDE 44 69 Melittin.
 FT MOD_RES 69 69 Glutamine amide (G-70 provides amide
 group) (By similarity).
 FT SEQUENCE 70 AA; 7585 MW; 607F52C091C23BB6 CRC64;
 SQ
 Query Match 41.1%; Score 64.5; DB 1; Length 70;
 Best Local Similarity 84.2%; Pred. No. 0.32;
 Matches 16; Conservative 0; Mismatches 3; Gaps 1;
 QY 9 GIGAVLKVLKVLTTGLPAL 27
 Db 44 GIGA---VLKVLTTGLPAL 59

RESULT 5
 MEL_VESMG
 ID MEL_VESMG STANDARD; PRT; 70 AA.
 AC P68408; P59260;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Melittin precursor.
 GN Name=MELT;
 OS Vespa magnifica (Hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespula.
 OX NCBI_TaxID=202807;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC Tissue=Venom gland;
 RX PubMed=12939801;
 RA Shi W.J., Zhang S.F., Zhang C.-X., Cheng J.A.;
 RT Cloning and comparative analysis of the venom prepro-melittin genes
 from four wasp species.";
 RL Yi Chuan Xue Bao 30:555-559(2003).
 CC -1- FUNCTION: Main toxin of bee venom with strong hemolytic activity.
 CC Integrates into cell membranes and has multiple effects, probably,
 as a result of its interaction with negatively charged
 phospholipids. It inhibits well known transport pumps such as the
 Na(+)-K(+)-ATPase and the H(+)-K(+)-ATPase. Increases the
 permeability of cell membranes to ions, particularly Na(+) and
 indirectly Ca(2+), because of the Na(+)-Ca(2+)-exchange (By
 similarity).
 CC -1- SUBUNIT: Monomer and homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: Belongs to the melittin family.
 CC
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 use as long as its content is in no way modified and this statement is not
 removed.
 CC
 CC EMBL: AF487910; AAO12204.1; -; mRNA.
 CC HSP: P01501; 1BH1.
 CC InterPro: IPR002116; Melittin.
 CC Pfam: PF01372; Melittin; 1.
 CC ProDom: PD014636; Melittin; 1.
 KW Amidation; Cytolysis; Hemolysis; Signal; Toxin.
 FT SIGNAL 1 21
 FT PROPEP 22 43 Removed by a dipeptidylpeptidase (By
 similarity).
 FT PEPTIDE 44 69 Melittin.
 FT MOD_RES 69 69 Glutamine amide (G-70 provides amide
 group) (By similarity).
 FT SEQUENCE 70 AA; 7543 MW;
 SQ

Query Match 41.1%; Score 64.5; DB 1; Length 70;
 Best Local Similarity 84.2%; Pred. No. 0.32;
 Matches 16; Conservative 0; Mismatches 3; Gaps 1;

QY 9 GIGAVLKVLKVLTTGLPAL 27
 ||||| ||||| ||||| |||||
 Db 44 GIGA---VLKVLTTGLPAL 59

RESULT 6
 MEL_VESVN STANDARD; PRT; 70 AA.
 AC P68109; P59260;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Melittin precursor.
 GN Name=MELT;
 OS Vespa velutina nigrithorax (Hornet).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=202809;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RC TISSUE=Venom gland;
 RX PubMed=12939801;
 RA Shi W.J., Zhang S.F., Zhang C.-X., Cheng J.A.;
 RT "Cloning and comparative analysis of the venom prepro-melittin genes
 from four wasp species";
 RL Yi Chuan Xue Bao 30:555-559(2003).
 CC -!- FUNCTION: Main toxin of bee venom with strong hemolytic activity.
 CC Integrates into cell membranes and has multiple effects, probably,
 CC as a result of its interaction with negatively charged
 CC phospholipids. It inhibits well known transport pumps such as the
 CC Na(+)-K(+)-ATPase and the H(+)-K(+)-ATPase. Increases the
 CC permeability of cell membranes to ions, particularly Na(+) and
 CC indirectly Ca(2+), because of the Na(+)-Ca(2+)-exchange (By
 CC similarity).
 CC -!- SUBUNIT: Monomer and homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the melittin family.

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 use as long as its content is in no way modified and this statement is not
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 EMBL; AF487908; AA012202.1; -; mRNA.
 DR HSSP; P01501; 1BH1.
 DR InterPro; IPR002116; Melittin.
 DR Pfam; PF01372; Melittin; 1.
 DR ProDom; PD014636; Melittin; 1.
 DR Amigaion; Cytolysis; Hemolysis; Signal; Toxin.
 FT SIGNAL 21 21 By similarity.
 FT PROPEP 22 43 Removed by a dipeptidylpeptidase (By
 FT similarity).
 FT PEPTIDE 44 69 Melittin.
 FT MOD_RES 69 69 Glutamine amide (G-70 provides amide
 FT group) (By similarity).
 FT SEQUENCE 70 AA; 7543 MW; DAGB17C086C9560C CRC64;

Query Match 41.1%; Score 64.5; DB 1; Length 70;
 Best Local Similarity 84.2%; Pred. No. 0.32;
 Matches 16; Conservative 0; Mismatches 3; Gaps 1;

QY 9 GIGAVLKVLKVLTTGLPAL 27
 ||||| ||||| ||||| |||||
 Db 44 GIGA---VLKVLTTGLPAL 59

RESULT 7

MEL_APICE STANDARD; PRT; 77 AA.
 AC Q8LW54;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Melittin precursor.
 GN Name=MELT;
 OS Apis cerana (Indian honeybee).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 OC Apidae; Apis.
 OX NCBI_TaxID=7461;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Le H.O., Le B.T.;
 RT "Gene encoding melittin in honeybee Apis cerana collected in Hanoi
 Vietnam";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP PROTEIN SEQUENCE OF 51-76.
 RA Kreil G.;
 RT "Structure of melittin isolated from two species of honey bees";
 RL FEBS Lett. 33:241-244(1973).
 CC -!- FUNCTION: Main toxin of bee venom with strong hemolytic activity.
 CC Integrates into cell membranes and has multiple effects, probably,
 CC as a result of its interaction with negatively charged
 CC phospholipids. It inhibits well known transport pumps such as the
 CC Na(+)-K(+)-ATPase and the H(+)-K(+)-ATPase. Increases the
 CC permeability of cell membranes to ions, particularly Na+ and
 CC indirectly Ca(2+), because of the Na(+)-Ca(2+)-exchange (By
 CC similarity).
 CC -!- SUBUNIT: Monomer and homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the melittin family.
 CC -!- DATABASE: NAME=Protein Spotlight; NOTE=Issue 12 of July 2001;
 CC WWW="http://www.expasy.org/spotlight/back issues/sptl012.shtml".

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 EMBL; AJ489619; CAD33921.1; -; Genomic DNA.
 DR PIR; A01762; MEHBCI.
 DR HSSP; P01501; 1BH1.
 DR InterPro; IPR002116; Melittin.
 DR Pfam; PF01372; Melittin; 1.
 DR ProDom; PD014636; Melittin; 1.
 DR Amigaion; Cytolysis; Direct protein sequencing; Hemolysis; Signal;
 FT SIGNAL 1 30 Potential.
 FT PROPEP 31 50 Removed by a dipeptidylpeptidase (By
 FT similarity).
 FT PEPTIDE 51 76 Melittin.
 FT MOD_RES 76 76 Glutamine amide (G-77 provides amide
 FT group).
 FT SEQUENCE 77 AA; 8515 MW; 091BEF7CB6019374 CRC64;

Query Match 41.1%; Score 64.5; DB 1; Length 77;
 Best Local Similarity 84.2%; Pred. No. 0.35;
 Matches 16; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 9 GIGAVLKVLKVLTTGLPAL 27
 ||||| ||||| ||||| |||||
 Db 51 GIGA---VLKVLTTGLPAL 66

RESULT 8

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MEL_APIDO
ID MEL_APIDO STANDARD; PRT; 26 AA.
AC P01502;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Melittin.
DE Melittin precursor.
GN Name=MELT;
OS Apis dorsata (Giant honeybee).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7462;
RN [1]
RN PROTEIN SEQUENCE.
RX MEDLINE=75168194; PubMed=1093875; DOI=10.1016/0014-5793(75)81079-9;
RA Kreil G.;
RT "The structure of Apis dorsata melittin: phylogenetic relationships
between honeybees as deduced from sequence data.";
RL FEBS Lett. 54:100-102(1975).
CC -!- FUNCTION: Main toxin of bee venom with strong hemolytic activity.
Integrates into cell membranes and has multiple effects, probably,
as a result of its interaction with negatively charged
phospholipids. It inhibits well known transport pumps such as the
Na(+)-K(+)-ATPase and the H(+)-K(+)-ATPase. Increases the
permeability of cell membranes to ions, particularly Na+ and
indirectly Ca(2+), because of the Na(+)-Ca(2+)-exchange.
CC -!- SUBUNIT: Monomer and homotetramer (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland (Probable).
CC -!- SIMILARITY: Belongs to the melittin family.
CC -!- DATABASE: NAME=Protein Spotlight; NOTE=Issue 12 of July 2001;
WWW="http://www.expasy.org/spotlight/back issues/splt012.shtml".
CC -----
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removed.
CC -----
CC PIR; A01763; MEHBCD.
DR HSSP; P01501; 1BH1.
DR InterPro; IPR002116; Melittin.
DR Pfam; PF01372; Melittin; 1.
DR ProDom; PD014636; Melittin; 1.
KW Amidation; Cytolysis; Direct protein sequencing; Hemolysis; Toxin.
FT MOD_RES 26 26 Glutamic acid 1-amide.
SQ SEQUENCE 26 AA; 2848 MW; FIDA8F92514EP01C CRC64;

Query Match 37.9%; Score 59.5; DB 1; Length 26;
Best Local Similarity 73.7%; Pred. No. 0.63;
Matches 14; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 9 GIGAVLKVLKVLTTGLPAL 27
Db 1 GIGAVLKVLKVLTTGLPAL 16

RESULT 9
ID MEL_POLHE STANDARD; PRT; 70 AA.
AC P59261;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Melittin precursor.
GN Name=MELT;
OS Polistes hebraeus (Paper wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Polistes.
OX NCBI_TaxID=202806;
RN [1]

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RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Venom gland;
RX PubMed=12939801;
RA Shi W.J., Zhang S.F., Zhang C.-X., Cheng J.A.;
RT "Cloning and comparative analysis of the venom prepro-melittin genes
from four wasp species.";
RL Yi Chuan Xue Bao 30:555-559(2003).
CC -!- FUNCTION: Has strong hemolytic activity. Integrates into cell
membranes and has multiple effects, probably, as a result of its
interaction with negatively charged phospholipids. It inhibits
well known transport pumps such as the Na(+)-K(+)-ATPase and the
H(+)-K(+)-ATPase. Increases the permeability of cell membranes to
ions, particularly Na+ and indirectly Ca(2+), because of the
Na(+)-Ca(2+)-exchange (By similarity).
CC -!- SUBUNIT: Monomer and homotetramer (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the melittin family.
CC -----
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removed.
CC -----
CC EMBL; AF487909; AAO12203.1; -; mRNA.
DR HSSP; P01501; 1BH1.
DR InterPro; IPR002116; Melittin.
DR Pfam; PF01372; Melittin; 1.
DR ProDom; PD014636; Melittin; 1.
KW Amidation; Cytolysis; Hemolysis; Signal; Toxin.
FT SIGNAL 1 21 By similarity.
FT PROPEP 22 43 Removed by a dipeptidylpeptidase (By
similarity).
FT PEPTIDE 44 69 Melittin.
FT MOD_RES 69 69 Glutamine amide (G-70 provides amide
group) (By similarity).
SQ SEQUENCE 70 AA; 7513 MW; DA70167086C9560C CRC64;

Query Match 37.9%; Score 59.5; DB 1; Length 70;
Best Local Similarity 78.9%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 9 GIGAVLKVLKVLTTGLPAL 27
Db 44 GIGAVLKVLKVLTTGLPAL 59

RESULT 10
Q7WR49 BORBR
ID Q7WR49 BORBR PRELIMINARY; PRT; 445 AA.
AC Q7WR49;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable amino acid permease.
GN OrderedLocNames=BB0108;
OS Bordetella bronchiseptica
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RX STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham A., Bason N., Chervach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

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RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640437; CAE30609.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid-transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/permease1.
DR InterPro; IPR004841; Permease region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome.
SQ SEQUENCE 445 AA; 46269 MW; 32678AB73968A556 CRC64;

Query Match 37.9%; Score 59.5; DB 2; Length 445;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 14; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

QY 2 WKLFKKIGIGAVLKVLKVLTTGLPALK 29
Db 411 WSSARYAGVGLIG-LAVLAAGLPALRL 437

RESULT 11
ID Q7W281 BORPA PRELIMINARY; PRT; 445 AA.
AC Q7W281;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable amino acid permease.
GN OrderedLocusNames=BPP0109;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=2287954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norbertczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640423; CAE39850.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid-transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/permease1.
DR InterPro; IPR004841; Permease region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome.
SQ SEQUENCE 445 AA; 46239 MW; 3DC2901D89630FF7 CRC64;

Query Match 37.9%; Score 59.5; DB 2; Length 445;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 14; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

QY 2 WKLFKKIGIGAVLKVLKVLTTGLPALK 29
Db 411 WSSARYAGVGLIG-LAVLAAGLPALRL 437

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RESULT 12
Q6WIH1 ARTBE PRELIMINARY; PRT; 643 AA.
ID Q6WIH1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Metalloprotease MEP4.
GN Name=meP4;
OS Arthroderma benhamiae (Trichophyton mentagrophytes).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Onygenales; Arthrodermataceae; Arthroderma.
OX NCBI_TaxID=63400;
RN [1]
NUCLEOTIDE SEQUENCE.
RP PubMed=14766908; DOI=10.1099/mic.0.26690-0;
RX Jousson O., Lechenne B., Bontems O., Capoccia S., Mignon B.,
RA Barblan J., Quadroni M., Monod M.;
RT "Multiplication of an ancestral gene encoding secreted fungalsysin
RT preceded species differentiation in the dermatophytes Trichophyton and
RT Microsporum.";
RL Microbiology 150:301-310(2004).
DR EMBL; AY283576; AAQ21101.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001842; Peptidase M36.
DR InterPro; IPR006025; Pept M Zn_BS.
DR InterPro; IPR002016; Peroxidase.
DR InterPro; IPR011096; Propep_M4_M36.
DR Pfam; PF07504; Ftp; 1.
DR Pfam; PF02128; Peptidase M36; 1.
DR PRINTS; PR00999; FUNGALYSIN.
DR PROSITE; PS00435; PEROXIDASE 1; UNKNOWN 1.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
KW Metalloprotease; Protease.
SQ SEQUENCE 643 AA; 70641 MW; BDCE89F15EC36CEE CRC64;

Query Match 37.6%; Score 59; DB 2; Length 643;
Best Local Similarity 44.4%; Pred. No. 17;
Matches 16; Conservative 2; Mismatches 12; Indels 6; Gaps 1;

QY 2 WKLFKKIGIGAVLKVLKVLTTGLP-----ALKLTL 31
Db 543 WNLIDKHGKGNVTKRVLKNGVPTDGRHLAMKLV 578

RESULT 13
Q8NIJ4 TRIRU PRELIMINARY; PRT; 643 AA.
ID Q8NIJ4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative secreted metalloprotease 4.
GN Name=MEP4;
OS Trichophyton rubrum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Onygenales; Arthrodermataceae; mitosporic Arthrodermataceae;
OC Trichophyton.
OX NCBI_TaxID=5551;
RN [1]
NUCLEOTIDE SEQUENCE.
RP PubMed=14766908; DOI=10.1099/mic.0.26690-0;
RX Jousson O., Lechenne B., Bontems O., Capoccia S., Mignon B.,
RA Barblan J., Quadroni M., Monod M.;
RT "Multiplication of an ancestral gene encoding secreted fungalsysin
RT preceded species differentiation in the dermatophytes Trichophyton and
RT Microsporum.";
RL Microbiology 150:301-310(2004).

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RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Capoccia S., Lechenne B., Zaugg C., Monod M.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407191; AAN03642.1; -; Genomic_DNA.
DR EMBL; AF407192; AAN03643.1; -; mRNA.
DR MEROPS; M36.001; -.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001842; Peptidase_M36.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR002016; Peroxidase.
DR InterPro; IPR011096; Propep_M4_M36.
DR Pfam; PF07504; FTP; 1.
DR Pfam; PF02128; Peptidase_M36; 1.
DR PRINTS; PR00999; FUNGALYSIN.
DR PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Metalloprotease; Protease.
SQ SEQUENCE 643 AA; 70698 MW; 1A03A8CB4CC35A42 CRC64;

Query Match 35.7%; Score 56; DB 2; Length 643;
Best Local Similarity 38.9%; Pred.No. 46;
Matches 14; Conservative 4; Mismatches 12; Indels 6; Gaps 1;

QY 2 WKLFKKGIGAVLVKLVLTGTLPLKLT 31
DB 543 WNLIDHKGKGVTKIRPVLKNGVPTDGRHLAKIVL 578

RESULT 14
Q8GME1 STRGL PRELIMINARY; PRT; 1939 AA.
AC Q8GME1.
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyketide synthase.
OS Streptomyces globisporus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C-1027;
RX MEDLINE=22171413; PubMed=12183628; DOI=10.1126/science.1072110;
RA Liu W., Christenson S.D., Standage S., Shen B.;
RL "Biosynthesis of the enediynes antitumor antibiotic C-1027."
RL Science 297:1170-1173(2002).
DR EMBL; AY048670; AAL06699.1; -; Genomic_DNA.
DR HSP; P25715; 1MLA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR009081; ACP like.
DR InterPro; IPR001227; Ac transferase.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00698; Acyl_transf_1; 1.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00109; ketoacyl-synt; 1.
DR Pfam; PF02801; Ketoacyl-synt C; 1.
SQ SEQUENCE 1939 AA; 203401 MW; 5CB272880237CC1P CRC64;

Query Match 35.7%; Score 56; DB 2; Length 1939;
Best Local Similarity 50.0%; Pred.No. 1.4e+02;
Matches 13; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 LFKKIGIGAVLVKLVLTGTLPLKLT 29
DB 829 LFEVGPGRVLSVLAETAGKPAVAL 854
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RESULT 15
Q84HN8 9ACTO PRELIMINARY; PRT; 1956 AA.
AC Q84HN8.
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PKsE.
GN Name=pkse;
OS Streptomyces ghanaensis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=35758;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NRRL B-12104;
RX MEDLINE=22447897; PubMed=12536216; DOI=10.1038/nbt784;
RA Zazopoulos E., Huang K., Staffa A., Liu W., Bachmann B.O., Nonaka K.,
RA Ahlert J., Thorson J.S., Shen B., Farnet C.M.;
RT "A genomics-guided approach for discovering and expressing cryptic
RT metabolic pathways."
RL Nat. Biotechnol. 21:187-190(2003).
DR EMBL; AF546141; AAO25844.1; -; Genomic_DNA.
DR HSP; P72391; 1NM2.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR009081; ACP like.
DR InterPro; IPR001227; Ac transferase.
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR000794; Ketoacyl synth.
DR Pfam; PF00698; Acyl_transf_1; 1.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00109; ketoacyl-synt; 1.
DR Pfam; PF02801; Ketoacyl-synt C; 1.
SQ SEQUENCE 1956 AA; 206626 MW; 8D24A06B63524824 CRC64;

Query Match 35.7%; Score 56; DB 2; Length 1956;
Best Local Similarity 50.0%; Pred.No. 1.4e+02;
Matches 13; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 4 LFKKIGIGAVLVKLVLTGTLPLKLT 29
DB 826 LFEVGPGRVLSGLARATTGVPVAL 851

Search completed: January 13, 2006, 11:57:45
Job time : 73 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2006, 11:56:06 ; Search time 61 Seconds
(without alignments)
219.189 Million cell updates/sec

Title: US-10-823-425-6
Perfect score: 157
Sequence: 1 KWKLKKIGIGAVLKVLKLTGLPALKLTLK 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pep:
2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pep:
4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep:
5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep:
6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	157	100.0	32	3	US-09-908-139-6
2	157	100.0	32	4	US-10-823-425-6
3	152	96.8	33	3	US-09-908-139-9
4	152	96.8	33	4	US-10-823-425-9
5	142.5	90.8	31	3	US-09-908-139-8
6	142.5	90.8	31	4	US-10-823-425-8
7	141	89.8	30	3	US-09-908-139-7
8	141	89.8	30	4	US-10-823-425-7
9	126.5	80.6	1105	5	US-10-845-936A-33
10	123.5	78.7	28	3	US-09-909-652-7
11	123.5	78.7	28	3	US-09-030-619-121
12	123.5	78.7	28	3	US-09-908-139-1
13	123.5	78.7	28	4	US-10-229-368-134
14	123.5	78.7	28	4	US-10-225-087-112
15	123.5	78.7	28	4	US-10-277-232-121
16	123.5	78.7	28	4	US-10-277-233-121
17	123.5	78.7	28	4	US-10-421-635-2
18	123.5	78.7	28	4	US-10-823-425-1
19	123.5	78.7	28	5	US-10-865-687-112
20	123.5	78.7	34	4	US-10-421-635-4
21	117.5	74.8	28	4	US-10-272-248-37
22	110	70.1	30	3	US-09-908-139-11
23	110	70.1	30	4	US-10-823-425-11
24	109.5	69.7	26	3	US-09-030-619-120
25	109.5	69.7	26	3	US-09-904-753-13
26	109.5	69.7	26	4	US-10-229-368-133
27	109.5	69.7	26	4	US-10-225-087-111

28 109.5 69.7 26 4 US-10-272-248-36
29 109.5 69.7 26 4 US-10-277-232-120
30 109.5 69.7 26 4 US-10-277-233-120
31 109.5 69.7 26 5 US-10-865-687-111
32 91.5 58.3 26 4 US-10-272-248-11
33 81.5 51.9 28 4 US-10-308-905A-40
34 81.5 51.9 28 4 US-10-661-471-40
35 74.5 47.5 1027 5 US-10-845-936A-32
36 65 41.4 15 3 US-09-820-053A-33
37 65 41.4 15 4 US-10-109-171-33
38 65 41.4 15 5 US-10-839-525-33
39 65 41.4 15 6 US-11-066-697-1036
40 65 41.4 15 6 US-11-136-186-33
41 64.5 41.1 22 4 US-10-609-217-514
42 64.5 41.1 22 4 US-10-632-388-514
43 64.5 41.1 22 4 US-10-651-723-514
44 64.5 41.1 22 4 US-10-645-761-514
45 64.5 41.1 22 4 US-10-666-696-514

ALIGNMENTS

RESULT 1
US-09-908-139-6
; Sequence 6, Application US/09908139
; Publication No. US20030096949A1
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/908,139
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/143,124
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-908-139-6
Query Match 100.0%; Score 157; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.3e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KWKLKKIGIGAVLKVLKLTGLPALKLTLK 32
DB 1 KWKLKKIGIGAVLKVLKLTGLPALKLTLK 32
RESULT 2
US-10-823-425-6
; Sequence 6, Application US/10823425
; Publication No. US20040186272A1
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/10/823,425

RESULT 6
US-10-823-425-8
; Sequence 8, Application US/10823425
; Publication No. US20040186272A1
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/10/823, 425
; CURRENT FILING DATE: 2004-04-12
; PRIORITY APPLICATION NUMBER: US/09/143,124

; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-10-823-425-8

Query Match 90.8%; Score 142.5; DB 4; Length 31;
Best Local Similarity 96.9%; Pred. No. 4.9e-13;
Matches 31; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 KWLKFKKIGIGAVLKVLTGTPALKLTLLK 32
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Db 1 KWK-FKKIGIGAVLKVLTGTPALKLTLLK 31

RESULT 7
US-09-908-139-7
; Sequence 7, Application US/09908139
; Publication No. US20030096949A1
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/908,139
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/143,124
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-908-139-7

Query Match 89.8%; Score 141; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.8e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KLPFKKIGIGAVLKVLTGTPALKLTLLK 32
|||
Db 1 KLPFKKIGIGAVLKVLTGTPALKLTLLK 30

RESULT 8
US-10-823-425-7
; Sequence 7, Application US/10823425
; Publication No. US20040186272A1
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/10/823,425
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/143,124
; PRIOR FILING DATE: 1998-08-28

; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-10-823-425-7

Query Match 89.8%; Score 141; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.8e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KLPFKKIGIGAVLKVLTGTPALKLTLLK 32
|||
Db 1 KLPFKKIGIGAVLKVLTGTPALKLTLLK 30

RESULT 9
US-10-845-936A-33
; Sequence 33, Application US/10845936A
; Publication No. US20040234609A1
; GENERAL INFORMATION:
; APPLICANT: Collier, Katherine D.
; APPLICANT: Cuevas, William A.
; APPLICANT: Kumar, Manoj A.
; TITLE OF INVENTION: Repeat Sequence Protein Polymer Active Agent Conjugates, Methods
; FILE REFERENCE: DOC0068PA/DC5058/GC792
; CURRENT APPLICATION NUMBER: US/10/845,936A
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: 60/470,464
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 1105
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: silk, elastin and MBI peptide repeats
US-10-845-936A-33

Query Match 80.6%; Score 126.5; DB 5; Length 1105;
Best Local Similarity 87.5%; Pred. No. 4.7e-09;
Matches 28; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
QY 1 KWLKFKKIGIGAVLKVLTGTPALKLTLLK 32
|||
Db 190 KWLKFKKIGIGA--VLKVLTTGLPALKLTLLK 218

RESULT 10
US-09-909-652-7
; Sequence 7, Application US/09909652
; Patent No. US2002025537A1
; GENERAL INFORMATION:
; APPLICANT: Kairos Scientific, Inc.
; APPLICANT: Bylina, Edward J.
; APPLICANT: Coleman, William J.
; APPLICANT: Youvan, Douglas C.
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR GENERATING
; FILE REFERENCE: 22346-7001
; CURRENT APPLICATION NUMBER: US/09/909,652
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/219,179
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 28

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CEMA analogue of cecropin-melittin hybrid
US-09-909-652-7

Query Match      78.7%; Score 123.5; DB 3; Length 28;
Best Local Similarity 90.0%; Pred. No. 2.3e-10;
Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KWKLFKKIGIGAVLVKLVLTGTPALKLT 30
   ||||| ||||| ||||| ||||| |||||
Db 1 KWKLFKKIGIGA---VLKVLTTGLPALKLT 27

RESULT 11
US-09-030-619-121
; Sequence 121, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Frazer, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 121
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-121

Query Match      78.7%; Score 123.5; DB 3; Length 28;
Best Local Similarity 90.0%; Pred. No. 2.3e-10;
Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KWKLFKKIGIGAVLVKLVLTGTPALKLT 30
   ||||| ||||| ||||| ||||| |||||
Db 1 KWKLFKKIGIGA---VLKVLTTGLPALKLT 27

RESULT 12
US-09-908-139-1
; Sequence 1, Application US/0908139
; Publication No. US20030096949A1
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/908,139
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/143,124
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-908-139-1

Query Match      78.7%; Score 123.5; DB 3; Length 28;
Best Local Similarity 90.0%; Pred. No. 2.3e-10;
Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KWKLFKKIGIGAVLVKLVLTGTPALKLT 30
   ||||| ||||| ||||| ||||| |||||
Db 1 KWKLFKKIGIGA---VLKVLTTGLPALKLT 27

RESULT 13
US-10-229-368-134
; Sequence 134, Application US/10229368
; Publication No. US20030148945A1
; GENERAL INFORMATION:
; APPLICANT: McNicol, Patricia J.
; APPLICANT: Pawlak, Sonia K.
; APPLICANT: Rubinchik, Evelina
; APPLICANT: Cameron, Dale
; APPLICANT: Guarina, Maria Marta
; TITLE OF INVENTION: ANTIMICROBIAL AND ANTI-INFLAMMATORY
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 660081.418
; CURRENT APPLICATION NUMBER: US/10/229,368
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Indolicidin peptide analogs
US-10-229-368-134

Query Match      78.7%; Score 123.5; DB 4; Length 28;
Best Local Similarity 90.0%; Pred. No. 2.3e-10;
Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KWKLFKKIGIGAVLVKLVLTGTPALKLT 30
   ||||| ||||| ||||| ||||| |||||
Db 1 KWKLFKKIGIGA---VLKVLTTGLPALKLT 27

RESULT 14
US-10-225-087-112
; Sequence 112, Application US/10225087
; Publication No. US20030171281A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: McNicol, Patricia J.
; APPLICANT: Frazer, Janet R.
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES AND
; TITLE OF INVENTION: FORMULATIONS THEREOF
; FILE REFERENCE: 660081.417
; CURRENT APPLICATION NUMBER: US/10/225,087
; CURRENT FILING DATE: 2003-01-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Indolicidin analog
US-10-225-087-112

Query Match      78.7%; Score 123.5; DB 4; Length 28;
Best Local Similarity 90.0%; Pred. No. 2.3e-10;
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Query Match 78.7%; Score 123.5; DB 4; Length 28;
Best Local Similarity 90.0%; Pred. NO. 2.3e-10;
Matches 27; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Search completed: January 13, 2006, 12:00:51
Job time : 61 secs

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OM protein - protein search, using sw model

Run on: January 13, 2006, 11:59:47 ; Search time 29 Seconds
(without alignments)
10.432 Million cell updates/sec

Title: US-10-823-425-6
Perfect score: 157
Sequence: 1 KWLKFKIGIGAVLVKLVLTGLPALKLTIX 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64.5	41.1	20	7 US-11-032-698A-2	Sequence 2, Appli
2	64.5	41.1	26	7 US-11-068-783-97	Sequence 97, Appl
3	64.5	41.1	26	7 US-11-032-698A-1	Sequence 1, Appli
4	64.5	41.1	26	7 US-11-123-182-7	Sequence 7, Appli
5	64.5	41.1	26	7 US-11-220-439-27	Sequence 27, Appl
6	64.5	41.1	28	7 US-11-123-182-11	Sequence 11, Appl
7	64.5	41.1	30	7 US-11-123-182-12	Sequence 12, Appl
8	62.5	39.8	38	7 US-11-123-182-2	Sequence 2, Appli
9	54.5	34.7	26	6 US-10-444-662-4	Sequence 4, Appli
10	52.5	33.4	535	7 US-11-114-906-16	Sequence 16, Appl
11	52.5	33.4	548	7 US-11-114-906-14	Sequence 14, Appl
12	52.5	33.4	648	7 US-11-114-906-12	Sequence 12, Appl
13	52.5	33.4	654	7 US-11-114-906-10	Sequence 10, Appl
14	52.5	33.4	751	7 US-11-114-906-8	Sequence 8, Appli
15	52.5	33.4	764	7 US-11-114-906-6	Sequence 6, Appli
16	52.5	33.4	776	7 US-11-114-906-24	Sequence 24, Appl
17	52.5	33.4	789	7 US-11-114-906-22	Sequence 22, Appl
18	52.5	33.4	838	7 US-11-114-906-40	Sequence 40, Appl
19	52.5	33.4	851	7 US-11-114-906-38	Sequence 38, Appl
20	52.5	33.4	863	7 US-11-114-906-32	Sequence 32, Appl
21	52.5	33.4	864	7 US-11-114-906-4	Sequence 4, Appli
22	52.5	33.4	870	7 US-11-114-906-2	Sequence 2, Appli
23	52.5	33.4	876	7 US-11-114-906-30	Sequence 30, Appl
24	52.5	33.4	889	7 US-11-114-906-20	Sequence 20, Appl
25	52.5	33.4	895	7 US-11-114-906-18	Sequence 18, Appl

26	52.5	33.4	951	7 US-11-114-906-36	Sequence 36, Appl
27	52.5	33.4	957	7 US-11-114-906-34	Sequence 34, Appl
28	52.5	33.4	976	7 US-11-114-906-28	Sequence 28, Appl
29	52.5	33.4	982	7 US-11-114-906-26	Sequence 26, Appl
30	51	32.5	1099	6 US-10-873-528-11	Sequence 11, Appl
31	47	29.9	171	6 US-10-793-626-1590	Sequence 1590, Ap
32	45.5	29.0	396	7 US-11-074-176-346	Sequence 346, App
33	45.5	29.0	405	7 US-11-074-176-164	Sequence 164, App
34	45	28.7	37	7 US-11-068-783-57	Sequence 57, Appl
35	45	28.7	37	7 US-11-123-182-4	Sequence 4, Appli
36	45	28.7	218	7 US-11-082-389-318	Sequence 318, App
37	45	28.7	446	7 US-11-082-389-316	Sequence 316, App
38	44.5	28.3	227	6 US-10-467-657-970	Sequence 970, App
39	44	28.0	69	6 US-10-846-479-4	Sequence 4, Appli
40	44	28.0	375	6 US-10-467-657-4766	Sequence 4766, Ap
41	43.5	27.7	307	7 US-11-082-389-4	Sequence 4, Appli
42	43.5	27.7	2312	7 US-11-126-313-34	Sequence 34, Appl
43	43	27.4	35	7 US-11-123-182-5	Sequence 5, Appli
44	43	27.4	564	7 US-11-082-389-78	Sequence 78, Appl
45	43	27.4	858	6 US-10-613-744-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-11-032-698A-2
; Sequence 2, Application US/11032698A
; Publication No. US20050266428A1
; GENERAL INFORMATION:
; APPLICANT: Monash University
; APPLICANT: LEE, Tzong-Hsien
; APPLICANT: AGUILAR, Marie-Isabel
; APPLICANT: PERLMUTTER, Patrick
; TITLE OF INVENTION: Purification Methods
; FILE REFERENCE: U015554-6
; CURRENT APPLICATION NUMBER: US/11/032,698A
; CURRENT FILING DATE: 2004-12-29
; PRIOR APPLICATION NUMBER: PCT/AU2003/000850
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-032-698A-2

Query Match 41.1%; Score 64.5; DB 7; Length 20;
Best Local Similarity 84.2%; Pred. No. 0.00079;
Matches 16; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 9 GIGAVLVKLVLTGLPAL 27
DB 1 GIGA---VLKVLTTGLPAL 16

RESULT 2
US-11-068-783-97
; Sequence 97, Application US/11068783
; Publication No. US20050260715A1
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Bartfield, Daniel
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS
; FILE REFERENCE: 660081.411
; CURRENT APPLICATION NUMBER: US/11/068,783
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/09/444,281
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 97
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Apis mellifera
US-11-068-783-97

Query Match 41.1%; Score 64.5; DB 7; Length 26;
Best Local Similarity 84.2%; Pred. No. 0.0011;
Matches 16; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 9 GIGAVLKVLKVLTTGLPAL 27
||| |||||
DB 1 GIGA---VLKVLTTGLPAL 16

RESULT 3

US-11-032-698A-1
; Sequence 1, Application US/11032698A
; Publication No. US20050266428A1
; GENERAL INFORMATION:
; APPLICANT: Monash University
; APPLICANT: LEE, Tzong-Hsien
; APPLICANT: AGUILAR, Marie-Isabel
; APPLICANT: PERLMUTTER, Patrick
; TITLE OF INVENTION: Purification Methods
; FILE REFERENCE: U015554-6
; CURRENT APPLICATION NUMBER: US/11/032,698A
; PRIOR FILING DATE: 2004-12-29
; PRIOR APPLICATION NUMBER: PCT/AU2003/000850
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-032-698A-1

Query Match 41.1%; Score 64.5; DB 7; Length 26;
Best Local Similarity 84.2%; Pred. No. 0.0011;
Matches 16; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 9 GIGAVLKVLKVLTTGLPAL 27
||| |||||
DB 1 GIGA---VLKVLTTGLPAL 16

RESULT 4

US-11-123-182-7
; Sequence 7, Application US/11123182
; Publication No. US20050267031A1
; GENERAL INFORMATION:
; APPLICANT: YU, XIANXANG
; APPLICANT: WAGNER, THOMAS E.
; TITLE OF INVENTION: THERAPEUTIC PORE-FORMING PEPTIDES
; FILE REFERENCE: 035879/0122
; CURRENT APPLICATION NUMBER: US/11/123,182
; PRIOR FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: US/09/851,422
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/203,063
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/212,042
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Apis mellifera
US-11-123-182-7

Query Match 41.1%; Score 64.5; DB 7; Length 26;

Best Local Similarity 84.2%; Pred. No. 0.0011;
Matches 16; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 9 GIGAVLKVLKVLTTGLPAL 27
||| |||||
DB 1 GIGA---VLKVLTTGLPAL 16

RESULT 5

US-11-220-439-27
; Sequence 27, Application US/11220439
; Publication No. US20060003938A1
; GENERAL INFORMATION:
; APPLICANT: Olivos Jr., Laszlo
; TITLE OF INVENTION: Novel Pyrrhocoricin-Derived Peptides, and Methods of
; FILE REFERENCE: WST91BUSA
; CURRENT APPLICATION NUMBER: US/11/220,439
; CURRENT FILING DATE: 2005-09-07
; PRIOR APPLICATION NUMBER: US/09/980,804
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/140,606
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/154,135
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Melittin
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (26)
; OTHER INFORMATION: AMIDATION
US-11-220-439-27

Query Match 41.1%; Score 64.5; DB 7; Length 26;
Best Local Similarity 84.2%; Pred. No. 0.0011;
Matches 16; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 9 GIGAVLKVLKVLTTGLPAL 27
||| |||||
DB 1 GIGA---VLKVLTTGLPAL 16

RESULT 6

US-11-123-182-11
; Sequence 11, Application US/11123182
; Publication No. US20050267031A1
; GENERAL INFORMATION:
; APPLICANT: YU, XIANXANG
; APPLICANT: WAGNER, THOMAS E.
; TITLE OF INVENTION: THERAPEUTIC PORE-FORMING PEPTIDES
; FILE REFERENCE: 035879/0122
; CURRENT APPLICATION NUMBER: US/11/123,182
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: US/09/851,422
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/203,063
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/212,042
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:

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; NAME/KEY: MOD RES
; LOCATION: (22)
; OTHER INFORMATION: [epsilon-gamma]-Glu
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (25)
; OTHER INFORMATION: [epsilon-gamma]-Glu
US-11-123-182-11

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Query Match 41.1%; Score 64.5; DB 7; Length 28;
Best Local Similarity 84.2%; Pred. No. 0.0012;
Matches 16; Conservative 0; Mismatches 0; Indels

Qy 9 GIGAVLKVLKVLTTGLPAL 27
||| |||||
Db 1 GIGAVLKVLKVLTTGLPAL 16

```

RESULT 7
US-11-123-182-12
; Sequence 12, Application US/11123182
; Publication No. US20050267031A1
; GENERAL INFORMATION:
; APPLICANT: YU, XIANXIANG
; APPLICANT: WAGNER, THOMAS E.
; TITLE OF INVENTION: THERAPEUTIC PORE-FORMING PEPTIDES
; FILE REFERENCE: 035879/0122
; CURRENT APPLICATION NUMBER: US/11/123,182
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: US/09/851,422
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/203,063
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/212,042
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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Query Match 41.1%; Score 64.5; DB 7; Length 30;
Best Local Similarity 84.2%; Pred. No. 0.0013;
Matches 16: Conservative 0; Mismatches 0; Indels

Qy 9 GIGAVLKVLTGTPAL 27
||| |||
Db 1 GIGAVLKVLTGTPAL 16

RESULT 8
US-11-123-182-2
; Sequence 2, Application US/11123182
; Publication No. US20050267031A1
; GENERAL INFORMATION:
; APPLICANT: YU, XIANYANG
; APPLICANT: WAGNER, THOMAS E.
; TITLE OF INVENTION: THERAPEUTIC PORE FORMING PEPTIDES
; FILE REFERENCE: 035879/0122
; CURRENT APPLICATION NUMBER: US/11/123.182

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; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: US/09/851,422
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/203,063
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/212,042
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

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Query Match	39.8%	Score 62.5;	DB 7;	Length 38;
Best Local Similarity	80.0%;	Pred. No. 0.0034;		
Matches 16:	Conservative 0;	Mismatches 3;	Indels 1;	Gaps 1;

Qy 9 GIGAVLK-VLKVLTTGLPAL 27
|||
db 1 GIGAVLKXXXXVLTGLPAL 20

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RESULT 9
US-10-444-662-4
; Sequence 4, Application US/10444662
; Publication No. US20050250683A9
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Rozema, David
; APPLICANT: Wolff, Jon
; APPLICANT: Wakefield, Darren
; APPLICANT: Ekena, Kirk
; APPLICANT: Hagstrom, James
; TITLE OF INVENTION: Reversible Modification of Membrane Interaction
; FILE REFERENCE: Mirus.035.01
; CURRENT APPLICATION NUMBER: US/10/444,662
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Apis florea
US-10-444-662-4

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```
Query Match          34.7%; Score 54.5; DB 6; Length 26;
Best Local Similarity 68.4%; Pred. No. 0.032; 2; Indels 3; Gaps 1;
Matches 13; Conservative 1; Mismatches 2;

QY 9 GIGAVLKVLKVLTTGLPAL 27
    |||| :|||| |||||
Db 1 GIGA---ILKVLATGLPTL 16

RESULT 10
US-11-114-906-16
; Sequence 16, Application US/11114906
; Publication No. US20050266452A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fridde, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/11/114,906
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: US/10/413,437
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 535
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(535)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-114-906-16

Query Match          33.4%; Score 52.5; DB 7; Length 535;
Best Local Similarity 37.5%; Pred. No. 2.4;
Matches 12; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

QY 1 KWKLFKKI---GIGAVLKVLKVLTTGLPAL 29
    :||: ||| | : : : : |||
Db 20 RWKVLKKGGGGGEIYEAMDLTTRENVALKV 51

RESULT 11
US-11-114-906-14
; Sequence 14, Application US/11114906
; Publication No. US20050266452A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fridde, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/11/114,906
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: US/10/413,437
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 14
; LENGTH: 548
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(548)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-114-906-14

Query Match          33.4%; Score 52.5; DB 7; Length 548;
Best Local Similarity 37.5%; Pred. No. 2.5;
Matches 12; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

QY 1 KWKLFKKI---GIGAVLKVLKVLTTGLPAL 29
    :||: ||| | : : : : |||
Db 33 RWKVLKKGGGGGEIYEAMDLTTRENVALKV 64

RESULT 12
US-11-114-906-12
; Sequence 12, Application US/11114906
; Publication No. US20050266452A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fridde, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/11/114,906
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: US/10/413,437
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 648
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(648)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-114-906-12

Query Match          33.4%; Score 52.5; DB 7; Length 648;
Best Local Similarity 37.5%; Pred. No. 3;
Matches 12; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

QY 1 KWKLFKKI---GIGAVLKVLKVLTTGLPAL 29
    :||: ||| | : : : : |||
Db 133 RWKVLKKGGGGGEIYEAMDLTTRENVALKV 164

RESULT 13
US-11-114-906-10
; Sequence 10, Application US/11114906
; Publication No. US20050266452A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fridde, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/11/114,906
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: US/10/413,437
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; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 654
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(654)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-114-906-10
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Query Match 33.4%; Score 52.5; DB 7; Length 654;
Best Local Similarity 37.5%; Pred. No. 3;
Matches 12; Conservative 7; Mismatches 10; Indels 3; Gaps 1;
```

```
QY 1 KWKLFKKI---GIGAVLKVLVLTGTPALKL 29
DB 139 RWKVLKKGGGGFGIYEAMDLLTRENVALKV 170
```

```
RESULT 14
US-11-114-906-8
; Sequence 8, Application US/11114906
; Publication No. US20050266452A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fride, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/11/114,906
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: US/10/413,437
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 751
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(751)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-114-906-8
```

```
Query Match 33.4%; Score 52.5; DB 7; Length 751;
Best Local Similarity 37.5%; Pred. No. 3.6;
Matches 12; Conservative 7; Mismatches 10; Indels 3; Gaps 1;
```

```
QY 1 KWKLFKKI---GIGAVLKVLVLTGTPALKL 29
DB 20 RWKVLKKGGGGFGIYEAMDLLTRENVALKV 51
```

```
RESULT 15
US-11-114-906-6
; Sequence 6, Application US/11114906
; Publication No. US20050266452A1
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```
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fride, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/11/114,906
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: US/10/413,437
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 764
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(764)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-114-906-6

Query Match 33.4%; Score 52.5; DB 7; Length 764;
Best Local Similarity 37.5%; Pred. No. 3.7;
Matches 12; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

QY 1 KWKLFKKI---GIGAVLKVLVLTGTPALKL 29
DB 33 RWKVLKKGGGGFGIYEAMDLLTRENVALKV 64

Search completed: January 13, 2006, 12:09:52
Job time : 29 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using **frame_plus_p2n_model**

Run on: January 15, 2006, 18:04:23 ; Search time 2333 Seconds
(without alignments)
779.679 Million cell updates/sec

Title: US-10-823-425-6
Perfect score: 157
Sequence: 1 KWLFKKIGIGAVLVKLVLTGLPALKLTK 32

Scoring table:
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delopt 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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13: gb.vi.*
14: gb.htg.*
15: gb.pl.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123.5	78.7	105	6	AX146858 Sequence
2	120.5	76.8	87	6	AX146856 Sequence
3	109.5	69.7	104	6	AR021130 Sequence

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	ORIGIN	Alignment Scores:	Pred. No.:	Score:
AX146858	AX146858	Sequence 3 from Patent WO0136647.	AX146858	AX146858.1	GI:14346164	synthetic construct	synthetic construct	other sequences; artificial sequences.	1	Misra, S., Kay, W.D. and Ousky, M.	Transgenic plants exhibiting resistance to a broad spectrum of pathogens	Patent: WO 0136647-A 3 25-MAY-2001; UNIVERSITY OF VICTORIA INNOVATION AND DEVELOPMENT CORPORATION (CA)	Location/Qualifiers 1. .105 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Nucleic acid sequence encoding ECEMA"	6.66e-11	105	27
AX146858	AX146858	Sequence 3 from Patent WO0136647.	AX146858	AX146858.1	GI:14346164	synthetic construct	synthetic construct	other sequences; artificial sequences.	1	Misra, S., Kay, W.D. and Ousky, M.	Transgenic plants exhibiting resistance to a broad spectrum of pathogens	Patent: WO 0136647-A 3 25-MAY-2001; UNIVERSITY OF VICTORIA INNOVATION AND DEVELOPMENT CORPORATION (CA)	Location/Qualifiers 1. .105 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Nucleic acid sequence encoding ECEMA"	6.66e-11	105	27
AX146858	AX146858	Sequence 3 from Patent WO0136647.	AX146858	AX146858.1	GI:14346164	synthetic construct	synthetic construct	other sequences; artificial sequences.	1	Misra, S., Kay, W.D. and Ousky, M.	Transgenic plants exhibiting resistance to a broad spectrum of pathogens	Patent: WO 0136647-A 3 25-MAY-2001; UNIVERSITY OF VICTORIA INNOVATION AND DEVELOPMENT CORPORATION (CA)	Location/Qualifiers 1. .105 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Nucleic acid sequence encoding ECEMA"	6.66e-11	105	27

Percent Similarity:	90.00%	Conservative:	0
Best Local Similarity:	90.00%	Mismatches:	0
Query Match:	78.66%	Indels:	3
DB:	6	Gaps:	1

UUS-10-823-425-6 (1-32) x AX146858 (1-105)

Qy	1	Lys	Trp	Leu	Leu	Pro	Leu	Leu	Val	Leu	Val	Leu	Val	Leu	Val	Leu	20
Db	19	AA	TG	AA	AA	CT	GT	TC	AA	GA	GA	TC	CG	GC	GC	GC	69
Qy	21	Thr	Thr	Gly	Leu	Pro	Ala	Leu	Leu	Leu	Thr	30					
Db	70	AC	CA	CG	GT	CT	GC	CG	CG	CT	GA	AG	CT	AA	CT	AA	99

RESULT 2	AX146856	87 bp	DNA	linear	PAT 08-JUN-2001
LOCUS	AX146856				
DEFINITION	Sequence 1 from Patent WO0136647.				
ACCESSION	AX146856				
VERSION	AX146856.1	GI:14346163			
KEYWORDS	.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
	other sequences; artificial sequences.				

ORIGIN	peptide
Alignment Scores:	
Pred. NO.:	1.64e-10
Score:	120.50
Percent Similarity:	90.00%
Best Local Similarity:	86.67%
Query Match:	76.75%
DB:	6
	Gaps: 1
	Indels: 3
	Mismatches: 0
	Conservative: 1
	Matches: 26
	Length: 87

US-10-823-425-6 (1-32) x AX146856 (1-87)

Qy 1 LysTrpLysLeuPheLysLysLleGlyIleGlyAlaValLeuLysValLeu 20
Db 1 AATGGAAACTGTTCAGAGAAGATCGGCATCGCGCC-----GTGCTGAACCTGCTG 51
Qy 21 ThrThrGlyLeuProAlaLeuLysLeuThr 30
Db 52 ACCACCGGTCTGCCGCGCTGAAGCTAAT 81

RESULT 3	104 bp	DNA	linear	PAT 05-DEC-1998
AR021130				
LOCUS				
DEFINITION	Sequence 1 from patent US 5789377.			
ACCESSION	AR021130			
VERSION	AR021130.1			
KEYWORDS	GI:3975745			
SOURCE	Unknown.			
ORGANISM	Unknown.			

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

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source
1. .104
/organism="unknown"
/mol type="unassigned DNA"
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ORIGIN

Alignment Scores:	1.17e-08	Length:	104
Pred. No.:	109.50	Matches:	24
Score:	88.89%	Conservative:	0
Percent Similarity:	88.89%	Mismatches:	0
Best Local Similarity:	88.89%	Indels:	3
Query Match:	69.75%	Gaps:	1
DB:	6		

US-10-823-425-6 (1-32) x AR021130 (1-104)

Qy	1	LyfTtpLysLeuPheLysLysLeuGlyTlleGlyAlaValLeuLysValLeuLysValLeu	20
Db	17	AAATGAAACTGTTCAAGAAGATCGGCATCGCGCC-----GTGCTGAAGTGTG	67
Qy	21	ThrThrGlyLeuProAlaLeu	27
Db	68	ACCACCGGTCTGCGCGCGTGTG	88

RESULT 4					
I33686					
LOCUS	I33686	104 bp	DNA		
DEFINITION	Sequence 1 from patent US 5593866.				
ACCESSION	I33686				
VERSION	I33686.1				
KEYWORDS	. GI:1824477				
SOURCE	Unknown.				
ORGANISM	Unknown.				
			linear	PAT 06-FEB-1997	

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source
1. .104
/organism="unknown"
/mol type="unassigned DNA"
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TTC 10 833 425 C (1-33) x T22596 (1-104)

Qy	1	LysTrpLysLeuPheIysIysIleGlyIleGlyAlaValLeuIysValLeuIysValLeu
Db	17	AAATGGAAACTGTTCAAGAAAGATCGCATGGCGCC-----GTGCTGAAGTCTG
Qy	21	ThrThrGlyLeuProAlaLeu 27
Db	68	ATCATCGGCTCTTCGCGGCGCTG 88

RESULT 5					
I74637					
LOCUS	I74637				
DEFINITION	Sequence 1 from patent US 5688767.		104 bp	DNA	linear
ACCESSION	I74637				
VERSION	I74637.1	GI:3010778			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 104)				
	Hancock,R.E.W., Piers,K.L., Brown,M.H. and Kelly,N.				

TITLE Treatment of endotoxin-associated disorders with cationic peptides
JOURNAL Patent: US 5688767-A 1 18-NOV-1997;
FEATURES Location/Qualifiers

source
1. .104
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.17e-08 Length: 104
Score: 109.50 Matches: 24
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 88.89% Indels: 3
DB: 69.75% Gaps: 1

US-10-823-425-6 (1-32) x I74637 (1-104)

QY 1 LysTrpLysLeuPheLysLysIleGlyIleGlyAlaValLeuLysValLeu 20
|||||
Db 17 AAATGGAAACTGTTCAAGAGATCGGCATCGCGCC-----GTGCTGAAAGTGCTG 67
QY 21 ThrThrGlyLeuProAlaLeu 27
|||||
Db 68 ACCACCGGTCTGCGCGGCTG 88

RESULT 6

LOCUS I79683 104 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 1 from patent US 5707855.
ACCESSION I79683
VERSION I79683.1 GI:3207973

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 104)
AUTHORS Hancock,R.E.W., Piers,K.L. and Brown,M.H.
TITLE CEMA cationic peptide and polynucleotides encoding CEMA
JOURNAL Patent: US 5707855-A 1 13-JAN-1998;
FEATURES Location/Qualifiers

source
1. .104
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.17e-08 Length: 104
Score: 109.50 Matches: 24
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 88.89% Indels: 3
DB: 69.75% Gaps: 1

US-10-823-425-6 (1-32) x I79683 (1-104)

QY 1 LysTrpLysLeuPheLysLysIleGlyIleGlyAlaValLeuLysValLeu 20
|||||
Db 17 AAATGGAAACTGTTCAAGAGATCGGCATCGCGCC-----GTGCTGAAAGTGCTG 67
QY 21 ThrThrGlyLeuProAlaLeu 27
|||||
Db 68 ACCACCGGTCTGCGCGGCTG 88

RESULT 7

AR021131/c
LOCUS AR021131 112 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5789377.
ACCESSION AR021131

VERSION

AR021131.1 GI:3975746

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 112)
AUTHORS Hancock,R.E.W., Piers,K.L., Brown,M.H. and Kelly,N.
TITLE Treatment of endotoxin-associated disorders with cationic peptides
JOURNAL Patent: US 5789377-A 2 04-AUG-1998;
FEATURES Location/Qualifiers

source
1. .112
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.27e-08 Length: 112
Score: 109.50 Matches: 24
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 88.89% Indels: 3
DB: 69.75% Gaps: 1

US-10-823-425-6 (1-32) x AR021131 (1-112)

QY 1 LysTrpLysLeuPheLysLysIleGlyIleGlyAlaValLeuLysValLeu 20
|||||
Db 92 AAATGGAAACTGTTCAAGAGATCGGCATCGCGCC-----GTGCTGAAAGTGCTG 42
QY 21 ThrThrGlyLeuProAlaLeu 27
|||||
Db 41 ACCACCGGTCTGCGCGGCTG 21

RESULT 8

LOCUS I33687/c 112 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 2 from patent US 5593866.
ACCESSION I33687

VERSION

I33687.1 GI:1824478

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 112)
AUTHORS Hancock,R.E.W., Piers,K.L. and Brown,M.H.
TITLE Cationic peptides and method for production
JOURNAL Patent: US 5593866-A 2 14-JAN-1997;
FEATURES Location/Qualifiers

source
1. .112
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.27e-08 Length: 112
Score: 109.50 Matches: 24
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 88.89% Indels: 3
DB: 69.75% Gaps: 1

US-10-823-425-6 (1-32) x I33687 (1-112)

QY 1 LysTrpLysLeuPheLysLysIleGlyIleGlyAlaValLeuLysValLeu 20
|||||
Db 92 AAATGGAAACTGTTCAAGAGATCGGCATCGCGCC-----GTGCTGAAAGTGCTG 42
QY 21 ThrThrGlyLeuProAlaLeu 27
|||||
Db 41 ACCACCGGTCTGCGCGGCTG 21

RESULT 9

LOCUS I74638/c 112 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 2 from patent US 5688767.
ACCESSION I74638

VERSION

I74638.1 GI:3010779

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 112)
TREATMENT of endotoxin-associated disorders with cationic peptides
TITLE Patent: US 5688767-A 2 18-NOV-1997;
JOURNAL Location/Qualifiers
FEATURES
1..112
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.27e-08 Length: 112
Score: 109.50 Matches: 24
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 69.75% Indels: 3
DB: 6 Gaps: 1

US-10-823-425-6 (1-32) x I74638 (1-112)
QY 1 LysTrpLysLeuPheLysLysIleGlyIleGlyAlaValLeuLysValLeuLysValLeu 20
Db 92 AATGGAAACTGTTCAAGAGATCGGCATCGGCC-----GTGCTGAAAGTGCTG 42

QY 21 ThrThrGlyLeuProAlaLeu 27
Db 41 ACCACCGGTCGCGCGGCTG 21

RESULT 10
I79684/c
LOCUS 112 bp DNA linear PAT 10-JUN-1998

DEFINITION Sequence 2 from patent US 5707855.
ACCESSION I79684
VERSION I79684.1 GI:3207974

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 112)
AUTHORS Hancock,R.E.W., Piers,K.L. and Brown,M.H.
TITLE CEMA cationic peptide and polynucleotides encoding CEMA
JOURNAL Patent: US 5707855-A 2 13-JAN-1998;
FEATURES
1..112
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.27e-08 Length: 112
Score: 109.50 Matches: 24
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 69.75% Indels: 3
DB: 6 Gaps: 1

US-10-823-425-6 (1-32) x I79684 (1-112)
QY 1 LysTrpLysLeuPheLysLysIleGlyIleGlyAlaValLeuLysValLeuLysValLeu 20
Db 92 AATGGAAACTGTTCAAGAGATCGGCATCGGCC-----GTGCTGAAAGTGCTG 42

QY 21 ThrThrGlyLeuProAlaLeu 27
Db 41 ACCACCGGTCGCGCGGCTG 21

RESULT 10
I79684/c
LOCUS 112 bp DNA linear PAT 10-JUN-1998

DEFINITION Sequence 2 from patent US 5707855.
ACCESSION I79684
VERSION I79684.1 GI:3207974

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 112)
AUTHORS Hancock,R.E.W., Piers,K.L. and Brown,M.H.
TITLE CEMA cationic peptide and polynucleotides encoding CEMA
JOURNAL Patent: US 5707855-A 2 13-JAN-1998;
FEATURES
1..112
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.27e-08 Length: 112
Score: 109.50 Matches: 24
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 69.75% Indels: 3
DB: 6 Gaps: 1

US-10-823-425-6 (1-32) x I79684 (1-112)
QY 1 LysTrpLysLeuPheLysLysIleGlyIleGlyAlaValLeuLysValLeuLysValLeu 20
Db 92 AATGGAAACTGTTCAAGAGATCGGCATCGGCC-----GTGCTGAAAGTGCTG 42

QY 21 ThrThrGlyLeuProAlaLeu 27
Db 41 ACCACCGGTCGCGCGGCTG 21

RESULT 10
I79684/c
LOCUS 112 bp DNA linear PAT 10-JUN-1998

DEFINITION Sequence 2 from patent US 5707855.
ACCESSION I79684
VERSION I79684.1 GI:3207974

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 112)
AUTHORS Hancock,R.E.W., Piers,K.L. and Brown,M.H.
TITLE CEMA cationic peptide and polynucleotides encoding CEMA
JOURNAL Patent: US 5707855-A 2 13-JAN-1998;
FEATURES
1..112
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.27e-08 Length: 112
Score: 109.50 Matches: 24
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 69.75% Indels: 3
DB: 6 Gaps: 1

US-10-823-425-6 (1-32) x I79684 (1-112)
QY 1 LysTrpLysLeuPheLysLysIleGlyIleGlyAlaValLeuLysValLeuLysValLeu 20
Db 92 AATGGAAACTGTTCAAGAGATCGGCATCGGCC-----GTGCTGAAAGTGCTG 42

QY 21 ThrThrGlyLeuProAlaLeu 27
Db 41 ACCACCGGTCGCGCGGCTG 21

RESULT 11
PSP314920
LOCUS 242 bp DNA linear INV 15-APR-2005

DEFINITION Polistes sp. HQL-2001 for melt gene for melittin.
ACCESSION AJ314920
VERSION AJ314920.1 GI:14495011
KEYWORDS melittin; melt gene.
SOURCE Polistes sp. HQL-2001
ORGANISM Polistes sp. HQL-2001

REFERENCE 1
AUTHORS Le,H.Q.
JOURNAL Thesis (2001) Department of Lab. Molecular Microbiology, Institute of Biotechnology, Hanoi, Viet Nam
REFERENCE 2
AUTHORS Le,H.Q., Nguyen,H.M. and Le,B.T.
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 242)
AUTHORS Le,H.Q.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2001) Le H.Q., Laboratory of Molecular Microbiology, Institute of Biotechnology, Hoang Quoc Viet Road, Nghia Do, Cau gay, Hanoi, 10,000, VIET NAM

FEATURES
source
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/organism="Polistes sp. HQL-2001"
/mol_type="genomic DNA"
/db_xref="taxon:30210"
/country="Viet Nam:Nghia Do, Hanoi"
39..242
/gene="melt"
39..242
/gene="melt"
/codon_start=1
/product="melittin"
/protein_id="CAC42164.1"
/db_xref="GI:14495012"
/db_xref="GOA:Q95219"
/db_xref="InterPro:IPR002116"
/db_xref="UniProt/TreMBL:Q95219"
translation="MRKSKLYAKTFLAEATCKVLLCSKYQVHIANCSHVSVLIGIA
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159..239
/gene="melt"
/product="melittin"

gene
CDS
mat_peptide
ORIGIN
Alignment Scores:
Pred. No.: 0.238 Length: 242
Score: 66.50 Matches: 16
Percent Similarity: 85.00% Conservative: 1
Best Local Similarity: 80.00% Mismatches: 0
Query Match: 42.36% Indels: 3
DB: 2 Gaps: 1

US-10-823-425-6 (1-32) x PSP314920 (1-242)
QY 8 IleGlyIleGlyAlaValLeuLysValLeuLysValLeuThrThrGlyLeuProAlaLeu 27
Db 156 CTAGGAATTGGAGCA-----GTTCGAGAGTATTACACAGATTGCCAGCCCTC 206

RESULT 12
AR478972
LOCUS AR478972
DEFINITION Sequence 17 from patent US 669689.
ACCESSION AR478972
VERSION AR478972.1 GI:47237846
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Kim,J.H., Kang,M.H., Lee,J.H., Park,S.H., Lee,J.W., Hong,S.S. and Lee,H.S.

US-10-823-425-6 (1-32) x PSP314920 (1-242)
QY 8 IleGlyIleGlyAlaValLeuLysValLeuLysValLeuThrThrGlyLeuProAlaLeu 27
Db 156 CTAGGAATTGGAGCA-----GTTCGAGAGTATTACACAGATTGCCAGCCCTC 206

RESULT 12
AR478972
LOCUS AR478972
DEFINITION Sequence 17 from patent US 669689.
ACCESSION AR478972
VERSION AR478972.1 GI:47237846
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Kim,J.H., Kang,M.H., Lee,J.H., Park,S.H., Lee,J.W., Hong,S.S. and Lee,H.S.

US-10-823-425-6 (1-32) x PSP314920 (1-242)
QY 8 IleGlyIleGlyAlaValLeuLysValLeuLysValLeuThrThrGlyLeuProAlaLeu 27
Db 156 CTAGGAATTGGAGCA-----GTTCGAGAGTATTACACAGATTGCCAGCCCTC 206

RESULT 12
AR478972
LOCUS AR478972
DEFINITION Sequence 17 from patent US 669689.
ACCESSION AR478972
VERSION AR478972.1 GI:47237846
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Kim,J.H., Kang,M.H., Lee,J.H., Park,S.H., Lee,J.W., Hong,S.S. and Lee,H.S.

US-10-823-425-6 (1-32) x PSP314920 (1-242)
QY 8 IleGlyIleGlyAlaValLeuLysValLeuLysValLeuThrThrGlyLeuProAlaLeu 27
Db 156 CTAGGAATTGGAGCA-----GTTCGAGAGTATTACACAGATTGCCAGCCCTC 206

RESULT 12
AR478972
LOCUS AR478972
DEFINITION Sequence 17 from patent US 669689.
ACCESSION AR478972
VERSION AR478972.1 GI:47237846
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Kim,J.H., Kang,M.H., Lee,J.H., Park,S.H., Lee,J.W., Hong,S.S. and Lee,H.S.

US-10-823-425-6 (1-32) x PSP314920 (1-242)
QY 8 IleGlyIleGlyAlaValLeuLysValLeuLysValLeuThrThrGlyLeuProAlaLeu 27
Db 156 CTAGGAATTGGAGCA-----GTTCGAGAGTATTACACAGATTGCCAGCCCTC 206

RESULT 12
AR478972
LOCUS AR478972
DEFINITION Sequence 17 from patent US 669689.
ACCESSION AR478972
VERSION AR478972.1 GI:47237846
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Kim,J.H., Kang,M.H., Lee,J.H., Park,S.H., Lee,J.W., Hong,S.S. and Lee,H.S.

US-10-823-425-6 (1-32) x PSP314920 (1-242)
QY 8 IleGlyIleGlyAlaValLeuLysValLeuLysValLeuThrThrGlyLeuProAlaLeu 27
Db 156 CTAGGAATTGGAGCA-----GTTCGAGAGTATTACACAGATTGCCAGCCCTC 206

RESULT 12
AR478972
LOCUS AR478972
DEFINITION Sequence 17 from patent US 669689.
ACCESSION AR478972
VERSION AR478972.1 GI:47237846
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Kim,J.H., Kang,M.H., Lee,J.H., Park,S.H., Lee,J.W., Hong,S.S. and Lee,H.S.

US-10-823-425-6 (1-32) x PSP314920 (1-242)
QY 8 IleGlyIleGlyAlaValLeuLysValLeuLysValLeuThrThrGlyLeuProAlaLeu 27
Db 156 CTAGGAATTGGAGCA-----GTTCGAGAGTATTACACAGATTGCCAGCCCTC 206

TITLE Mass production method of antimicrobial peptide and DNA construct and expression system thereof

JOURNAL Patent: US 669689-A 17 02-MAR-2004; Samyang Genex Corporation; Chongno-ku; KRX;

FEATURES
source
 1. .48
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 0.0831 Length: 48
 Score: 64.50 Matches: 16
 Percent Similarity: 84.21% Conservative: 0
 Best Local Similarity: 84.21% Mismatches: 0
 Query Match: 41.08% Indels: 3
 DB: 6 Gaps: 1

US-10-823-425-6 (1-32) x AR478972 (1-48)

QY 9 GlyIleGlyAlaValLeuLysValLeuLysValLeuThrThrGlyLeuProAlaLeu 27

Db 1 GGTATCGGTGCG-----GTTCTGAAAGTTCTGACCACCGGTCTGCGGCGCTG 48

RESULT 13

A34185

LOCUS A34185 63 bp DNA linear PAT 03-JUL-2002

DEFINITION Synthetic human t-PA gene oligo.

ACCESSION A34185

VERSION A34185.1 GI:21694181

KEYWORDS synthetic construct

SOURCE other sequences; artificial sequences.

ORGANISM 1 (bases 1 to 63)

REFERENCE Mueller-Neumann, M., Schmidt, M., Schwarz, M., Baldinger, V., Doerper, I., Strube, K.H. and Bialojan, S.

AUTHORS Polypeptides, their preparation and their use

TITLE Patent: EP 0350692-A 16 17-JAN-1990;

JOURNAL BASF Aktiengesellschaft

FEATURES
source
 1. .63
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

ORIGIN

Alignment Scores:
 Pred. No.: 0.112 Length: 63
 Score: 64.50 Matches: 16
 Percent Similarity: 84.21% Conservative: 0
 Best Local Similarity: 84.21% Mismatches: 0
 Query Match: 41.08% Indels: 3
 DB: 6 Gaps: 1

US-10-823-425-6 (1-32) x A34185 (1-63)

QY 9 GlyIleGlyAlaValLeuLysValLeuLysValLeuThrThrGlyLeuProAlaLeu 27

Db 6 GGAAATGGACGAC-----GTACTGAAGATTATACACAGATTGCGCGCCCTC 53

RESULT 14

AR479002

LOCUS AR479002 88 bp DNA linear PAT 14-MAY-2004

DEFINITION Sequence 53 from patent US 669689.

ACCESSION AR479002

VERSION AR479002.1 GI:47237876

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 88)

AUTHORS Kim, J.H., Kang, M.H., Lee, J.H., Park, S.H., Lee, J.W., Hong, S.S. and Lee, H.S.

TITLE Mass production method of antimicrobial peptide and DNA construct and expression system thereof

JOURNAL Patent: US 669689-A 53 02-MAR-2004; Samyang Genex Corporation; Chongno-ku; KRX;

FEATURES
Location/Qualifiers
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 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 0.163 Length: 88
 Score: 64.50 Matches: 16
 Percent Similarity: 84.21% Conservative: 0
 Best Local Similarity: 84.21% Mismatches: 0
 Query Match: 41.08% Indels: 3
 DB: 6 Gaps: 1

US-10-823-425-6 (1-32) x AR479002 (1-88)

QY 9 GlyIleGlyAlaValLeuLysValLeuLysValLeuThrThrGlyLeuProAlaLeu 27

Db 1 GGTATCGGTGCG-----GTTCTGAAAGTTCTGACCACCGGTCTGCGGCGCTG 48

RESULT 15

AF487908

LOCUS AF487908 213 bp mRNA linear INV 25-DEC-2002

DEFINITION Vespa velutina nigrithorax prepromelittin mRNA, complete cds.

ACCESSION AF487908

VERSION AF487908.1 GI:27372434

KEYWORDS Vespa velutina nigrithorax

SOURCE Vespa velutina nigrithorax

ORGANISM Vespa velutina nigrithorax

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.

AUTHORS Shi, W.J., Zhang, S.F., Zhang, C.X. and Cheng, J.A.

TITLE Cloning and sequencing of cDNA coding for prepromelittin of Polistes hebraeus, Vespa magnifica and Vespa maculifrons

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 213)

AUTHORS Shi, W.J., Zhang, S.F., Zhang, C.X. and Cheng, J.A.

TITLE Direct Submission

JOURNAL Submitted (27-FEB-2002) Institute of Applied Entomology, Zhejiang University, KaiXuan Road268, Hangzhou, Zhejiang 310029, China

FEATURES
Location/Qualifiers
 1. .213
 /organism="Vespa velutina nigrithorax"
 /mol_type="mRNA"
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 /sex="female"
 /tissue_type="venom gland"
 1. .213
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 /product="prepromelittin"
 /protein_id="AA012202.1"
 /db_xref="GI:27372435"
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CDS

Alignment Scores:
 Pred. No.: 0.432 Length: 213
 Score: 64.50 Matches: 16
 Percent Similarity: 84.21% Conservative: 0
 Best Local Similarity: 84.21% Mismatches: 0
 Query Match: 41.08% Indels: 3
 DB: 2 Gaps: 1

US-10-823-425-6 (1-32) x AF487908 (1-213)

Qy	9	Gly	Ile	Gly	Ala	Val	Leu	Lys	Val	Leu	Thr	Thr	Gly	Leu	Pro	Ala	Leu	27
Db	130	GGA	ATT	GGA	GCA	-----	GTT	CTC	AAA	GTAT	TAA	CCAC	AGG	ATT	GCT	GCC	CTT	177

Search completed: January 15, 2006, 19:30:28
Job time : 2340 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 17:06:05 ; Search time 506 Seconds

(without alignments)
421.483 Million cell updates/sec

Title: US-10-823-425-6

Perfect score: 157

Sequence: 1 KWKLPKKGIGAVLVKLVLTGTPALKLTLK 32

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=tblastx -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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3: Geneseq2000s.*
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5: Geneseq2001bs.*
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7: Geneseq2002bs.*
8: Geneseq2003as.*
9: Geneseq2003bs.*
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11: Geneseq2003ds.*
12: Geneseq2004as.*
13: Geneseq2004bs.*
14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	109.5	69.7	104	AAT33488	Aat33488 104mer en
4	109.5	69.7	104	AAT63051	Aat63051 104-mer e

5	109.5	69.7	104	2	AAV10887	Aav10887 Human cec
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7	109.5	69.7	112	2	AAT63052	Aat63052 112-mer e
8	109.5	69.7	112	2	AAV10888	Aav10888 Human cec
9	70	44.6	78	11	ADM56051	Adm56051 Antibacte
10	70	44.6	762	11	ADM56057	Adm56057 GST-GK-1
11	64.5	41.1	48	3	Aaz29391	Aaz29391 PCR prime
12	64.5	41.1	48	6	ABL60416	Ab160416 DNA fragm
13	64.5	41.1	213	10	AAL56635	Aal56635 cDNA enco
14	64.5	41.1	213	10	ADL06283	Adl06283 cDNA enco
15	64	40.8	1245	10	ADB69787	Adb69787 C. neofo
16	60	38.2	1770	8	ACA36718	Aca36718 Prokaryot
17	60	38.2	110000	6	ABA03041_06	Continuation (7 of
18	59.5	37.9	88	3	Aaz29365	Aaz29365 Antimicro
19	59.5	37.9	88	6	ABL60446	Ab160446 DNA fragm
20	59.5	37.9	213	10	AAL56452	Aal56452 cDNA sequ
21	58.5	37.3	78	2	AAV83790	Aav83790 Antimicro
22	58	36.9	1447	13	ADX65253	Adx65253 Plant ful
23	58	36.9	3250	13	ADX60208	Adx60208 Plant ful
24	57	36.3	2823	13	ADX63183	Adx63183 Plant ful
25	57	36.3	4710	6	ABQ69266	Abq69266 Listeria
26	57	36.3	4710	6	ABQ67872	Abq67872 Listeria
27	57	36.3	81905	6	ABQ69244	Abq69244 Listeria
28	57	36.3	82689	6	ABQ67198	Abq67198 Listeria
29	56	35.7	277	12	ADP61467	Adp61467 Soybean c
30	56	35.7	2766	11	ADM02434	Adm02434 Human cDN
31	56	35.7	5871	6	ABS78666	Abs78666 S. ghanae
32	56	35.7	5871	14	ABE12628	Aeb12628 Sneydyne
33	56	35.7	5871	14	AEC10221	Aec10221 Streptomy
34	55.5	35.4	1356	9	ADB07623	Adb07623 Alloiococ
35	55.5	35.4	110000	9	ADB12064_03	Continuation (4 of
36	54	34.4	477	2	AAI4087	Aai4087 H. pylori
37	54	34.4	597	13	ADQ79367	Adq79367 Novel can
38	54	34.4	1377	9	ACC85181	Acc85181 Mangrove
39	54	34.4	109565	13	ABD33086	Abd33086 Murine ca
40	54	34.4	262090	12	ADQ59207	Adq59207 MSI-H car
41	53.5	34.1	480	2	AAI34103	Aai34103 Mycobacte
42	53.5	34.1	486	13	ADU16723	Adu16723 M. tuberc
43	53.5	34.1	498	2	AAI34104	Aai34104 Mycobacte
44	53.5	34.1	498	13	ADU16725	Adu16725 M. tuberc
45	53.5	34.1	33737	6	AAL50815	Aal50815 Human can

ALIGNMENTS

RESULT 1

AAH44807

ID AAH44807 standard; DNA; 105 BP.

XX

AC AAH44807;

XX

DT 30-AUG-2001 (first entry)

XX

DE DNA encoding antimicrobial ECEMA (extended cecropin-mellitin) peptide.

XX

KW Transgenic plant; cationic peptide; cecropin-mellitin; CEWA; resistance;
antibacterial; antifungal; antimicrobial; food crop; blight; soft rot;
ds.

XX

OS Synthetic.

XX

Key Location/Qualifiers

FT CDS

FT /tag= a

FT /product= "ECEMA"

FT /note= "Extended cecropin-mellitin peptide"

XX

PN WO200136647-A1.

XX

PD 25-MAY-2001.

XX

PF 14-JUL-2000; 2000WO-CA000826.

XX

```
PR 12-NOV-1999; 99US-0165249P.
XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
XX
XX
XX Misra S, Kay WD, Ousky M;
XX
XX WPI; 2001-336007/35.
XX P-PSDB; AAG62380.
XX
XX Transgenic plants useful as food crops are resistant to late blight due
XX to Phytophthora infestans and/or to soft rot due to Erwinia carotovora.
XX
XX Disclosure; Page 50; 55pp; English.
XX
XX The present invention relates to a transgenic plant, which expressed a
XX cationic peptide of the cecropin-mellitin (CEMA) family or related
XX peptide. CEMA is an antimicrobial peptide with confers resistance to
XX fungal and bacterial pathogens. Included in the invention are CEMA-
XX related fusion peptides in which an N-terminal extension peptide is fused
XX to the CEMA peptide. A pro-region peptide may be used as a fusion
XX peptide, which neutralises the cationic nature of the CEMA or CEMA-
XX related peptide and provides enhanced stability in cellular environments,
XX or decreases the toxicity of the CEMA or CEMA-related peptide to the host
XX organism. Transgenic plants of the invention may be used in conventional
XX agricultural applications, such as food crops. The plants may display
XX resistance to late blight due to Phytophthora infestans and or to soft
XX rot due to Erwinia carotovora. The present sequence represents DNA
XX encoding CEMA, an N-terminally extended CEMA peptide, which is used in
XX the production of the transgenic plants of the invention
XX
XX Sequence 105 BP; 30 A; 24 C; 30 G; 21 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 6.86e-12 Length: 105
Score: 123.50 Matches: 27
Percent Similarity: 90.00% Conservative: 0
Best Local Similarity: 90.00% Mismatches: 0
Query Match: 78.66% Indels: 3
DB: 4 Gaps: 1
XX
US-10-823-425-6 (1-32) x AAH44807 (1-105)
QY 1 LysTrpLysLeuPheIysLysIleGlyIleGlyAlaValLeuLysValLeu 20
Db 19 AAATGGAAACTGTTCAGGAAGATCGGCATCGGCC-----GTGCTGAAGTCTG 69
QY 21 ThrThrGlyLeuProAlaLeuLysLeuThr 30
Db 70 ACCACCGGTCTGCGGCGCTGAAGCTAACT 99
XX
RESULT 2
AAH44806
ID AAH44806 standard; DNA; 87 BP.
XX
XX AAH44806;
XX
XX 30-AUG-2001 (first entry)
XX
XX DNA encoding antimicrobial CEMA (cecropin-mellitin) peptide.
XX
XX Transgenic plant; cationic peptide; cecropin-mellitin; CEMA; resistance;
XX antibacterial; antifungal; antimicrobial; food crop; blight; soft rot;
XX ds.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 1..87
XX /*tag= a
XX /partial
XX /product= "CEMA"
XX /note= "Cecropin-mellitin peptide"
XX /transl_except= (pos:46..48, aa:Val)
XX
FT 12-NOV-1999; 99US-0165249P.
XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
XX
XX
XX Misra S, Kay WD, Ousky M;
XX
XX WPI; 2001-336007/35.
XX P-PSDB; AAG62379.
XX
XX Transgenic plants useful as food crops are resistant to late blight due
XX to Phytophthora infestans and/or to soft rot due to Erwinia carotovora.
XX
XX Disclosure; Page 49; 55pp; English.
XX
XX The present invention relates to a transgenic plant, which expressed a
XX cationic peptide of the cecropin-mellitin (CEMA) family or related
XX peptide. CEMA is an antimicrobial peptide with confers resistance to
XX fungal and bacterial pathogens. Included in the invention are CEMA-
XX related fusion peptides in which an N-terminal extension peptide is fused
XX to the CEMA peptide. A pro-region peptide may be used as a fusion
XX peptide, which neutralises the cationic nature of the CEMA or CEMA-
XX related peptide and provides enhanced stability in cellular environments,
XX or decreases the toxicity of the CEMA or CEMA-related peptide to the host
XX organism. Transgenic plants of the invention may be used in conventional
XX agricultural applications, such as food crops. The plants may display
XX resistance to late blight due to Phytophthora infestans and or to soft
XX rot due to Erwinia carotovora. The present sequence represents DNA
XX encoding CEMA, an N-terminally extended CEMA peptide, which is used in
XX the production of the transgenic plants of the invention
XX
XX Sequence 87 BP; 25 A; 23 C; 23 G; 16 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1.72e-11 Length: 87
Score: 120.50 Matches: 26
Percent Similarity: 90.00% Conservative: 1
Best Local Similarity: 86.67% Mismatches: 0
Query Match: 76.75% Indels: 3
DB: 4 Gaps: 1
XX
US-10-823-425-6 (1-32) x AAH44806 (1-87)
QY 1 LysTrpLysLeuPheIysLysIleGlyIleGlyAlaValLeuLysValLeu 20
Db 1 AAATGGAAACTGTTCAGGAAGATCGGCATCGGCC-----GTGCTGAAGTCTG 51
QY 21 ThrThrGlyLeuProAlaLeuLysLeuThr 30
Db 52 ACCACCGGTCTGCGGCGCTGAAGCTAACT 81
XX
RESULT 3
AAT33488
ID AAT33488 standard; DNA; 104 BP.
XX
XX AAT33488;
XX
XX 21-MAY-1997 (first entry)
XX
XX 104mer encoding CEME.
XX
XX Cationic peptide; CEMA; CEME; cecropia; melittin; bacterial growth;
XX antibiotic activity; permeable; bacterial outer membrane;
XX lipopolysaccharide; fusion peptide; inhibition; endotoxaemia;
XX sepsis associated disorder; septic shock; ss.
XX
```


OS Synthetic.
 XX W09628559-A1.
 XX
 XX 19-SEP-1996.
 XX
 XX 13-MAR-1996; 96WO-1B000431.
 XX PF
 XX 13-MAR-1995; 95US-00405234.
 XX PR
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 XX PA
 XX Hancock RW, Piers KL, Brown MH, Kelly N;
 XX PI
 XX WPI; 1996-433831/43.
 XX DR
 XX Recombinant production of antimicrobial, cationic peptide - produced in
 PT bacterial host as fusion peptide with an anionic portion for suppressing
 PT the anti-microbial activity of the cationic peptide.
 XX
 XX Example 2; Page 19; 90pp; English.
 XX
 CC The sequences given in AAT33488-500 and AAT40195-204 are oligonucleotides
 CC which were used in the construction of vectors used in the method of the
 CC invention. The method comprises constructing an expression vector
 CC containing DNA encoding the cationic peptide adjacent to DNA encoding an
 CC anionic carrier peptide which inhibits bacterial proteases. A bacterial
 CC host cell is transformed with the vector and cultured to express a fusion
 CC peptide comprising the cationic and anionic peptides. The biologically
 CC active cationic peptide is then recovered. The vectors constructed using
 CC these sequences encode CEME, CEMA or HNP-1 (human neutrophil peptide 1).
 CC CEMA contains the first 18 amino acids of cecropin A and the last 8
 CC residues of melittin. CEMA is derived from CEME by changing the C-
 CC terminal amino acid of CEME to include two additional lys residues. This
 CC modification improves the antibiotic activity of the peptide against many
 CC bacterial species, two fold, as well as substantially enhancing its
 CC ability to permeabilise bacterial outer membranes and to bind to
 CC lipopolysaccharide. CEMA and CEME act to permeabilise bacterial membranes
 CC breaking down the outer membrane permeability barrier. They may be used
 CC in conjunction with antibiotics to inhibit bacterial growth and to treat
 CC an endotoxaemia or sepsis associated disorders e.g. septic shock
 XX
 SQ Sequence 104 BP; 27 A; 26 C; 31 G; 20 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.52e-09 Length: 104
 Score: 109.50 Matches: 24
 Percent Similarity: 88.89% Conservative: 0
 Best Local Similarity: 88.89% Mismatches: 0
 Query Match: 69.75% Indels: 3
 DB: 2 Gaps: 1

US-10-823-425-6 (1-32) x AAT33488 (1-104)

QY 1 LysTTPlysLeuPhelLysLysIleGlyIleGlyAlaValLeuLysValLeu 20
 DB 17 AATATGAATCTGTTCAAGAAGATCGCATCGCGCC-----GTGCTGAAGTGTG 67

QY 21 ThrThrGlyLeuProAlaLeu 27
 DB 68 ACCACCGGTCTGCCGCGCTG 88

RESULT 4
 AAT63051
 ID AAT63051 standard; DNA; 104 BP.
 XX
 AC AAT63051;
 XX
 XX 25-MAR-2003 (revised)
 DT 08-MAY-1997 (first entry)
 XX
 XX 104-mer encoding CEME.

KW HNP-1; CEME; CEMA; human neutrophil protein; fusion; insect defensin;
 KW cecropin A; bee venom; melittin; antibiotic activity; S. typhimurium;
 KW permeability; bacterial outer membrane; lipopolysaccharide; antibiotic;
 KW E. coli; Pseudomonas aeruginosa; E. cloacae; S. aureus; ss.
 XX Synthetic.
 XX
 XX US5593866-A.
 XX PD
 XX 14-JAN-1997.
 XX
 XX 20-DEC-1995; 95US-00575052.
 XX PF
 XX 21-AUG-1992; 92US-00933492.
 XX PR
 XX 20-AUG-1993; 93US-00110502.
 XX
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 XX PA
 XX Brown MH, Piers KL, Hancock RW;
 XX PI
 XX WPI; 1997-099468/09.
 XX DR
 XX Prodn. of recombinant cationic peptide with antimicrobial activity - in
 PT the form of a fusion peptide with protease-inhibiting anionic peptide.
 PT
 XX Example 1; Col 9-10; 31pp; English.
 XX
 CC The sequences given in AAT63051-64 represent oligonucleotides which were
 CC used in the construction of pGST-petide plasmids for the expression of
 CC HNP-1, CEME and CEMA. HNP-1 is peptide 1 from human neutrophil protein,
 CC CEME is a fusion peptide made from portions of an insect defensin
 CC cecropin A and the bee venom peptide melittin, and CEMA is a variant of
 CC CEME with two additional lysine residues at the C-terminal end. The
 CC modification from CEME to CEMA causes a two-fold improvement in
 CC antibiotic activity against many bacterial species as well as
 CC substantially enhancing the ability to permeabilise bacterial outer
 CC membranes and binding to lipopolysaccharides. CEMA may be used
 CC synergistically with classical antibiotics to break down the outer
 CC membrane permeability barrier. It is possibly active against E. coli,
 CC Pseudomonas aeruginosa, E. cloacae, S. typhimurium and S. aureus.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 104 BP; 27 A; 26 C; 31 G; 20 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.52e-09 Length: 104
 Score: 109.50 Matches: 24
 Percent Similarity: 88.89% Conservative: 0
 Best Local Similarity: 88.89% Mismatches: 0
 Query Match: 69.75% Indels: 3
 DB: 2 Gaps: 1

US-10-823-425-6 (1-32) x AAT63051 (1-104)

QY 1 LysTTPlysLeuPhelLysLysIleGlyIleGlyAlaValLeuLysValLeu 20
 DB 17 AATATGAATCTGTTCAAGAAGATCGCATCGCGCC-----GTGCTGAAGTGTG 67

QY 21 ThrThrGlyLeuProAlaLeu 27
 DB 68 ACCACCGGTCTGCCGCGCTG 88

RESULT 5
 AAV10887
 ID AAV10887 standard; DNA; 104 BP.
 XX
 AC AAV10887;
 XX
 XX 14-JUL-1998 (first entry)
 DT
 XX Human cecropin A/melittin hybrid peptide primer 1.
 DE
 XX Cecropin A; melittin; CEME; fusion protein; polycationic; antibacterial;

KW permeable; outer membrane; lipopolysaccharide; bacterial infection;
 KW septic shock; primer; ss.
 OS Synthetic.
 OS Homo sapiens.
 PN US5707855-A.
 XX 13-JAN-1998.
 PD 20-DEC-1996; 96US-00770557.
 XX 21-AUG-1992; 92US-00933492.
 PR 20-AUG-1993; 93US-00110502.
 PR 20-DEC-1995; 95US-00575052.
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA Brown MH, Piers KL, Hancock REW;
 PI WPI; 1998-100348/09.
 XX Antibacterial peptide CEMA - useful for treating bacterial infections and
 PT septic shock.
 XX Example 1; Col 10; 31pp; English.
 PS AAV10887-V10909 are primers used in a method which allows the production
 CC of a novel polycationic antibacterial peptide, CEMA. This peptide is a is
 CC a hybrid comprising the first 18 amino acids of cecropin A and the last 8
 CC amino acids of melittin. It has two Lys residues at the C terminus which
 CC creates a sequence with two-fold increased antibiotic activity against
 CC many bacterial species as well as enhanced ability to permeabilise
 CC bacterial outer membranes and bind to lipopolysaccharide. CEMA can be
 CC used to treat bacterial infections and septic shock
 XX Sequence 104 BP; 27 A; 26 C; 31 G; 20 T; 0 U; 0 Other;
 SQ Alignment Scores: 1.52e-09 Length: 104
 Pred. No.: 109.50 Matches: 24
 Score: 88.89% Conservative: 0
 Percent Similarity: 88.89% Mismatches: 0
 Best Local Similarity: 88.89% Indels: 3
 Query Match: 69.75% Gaps: 1
 DB: 2
 US-10-823-425-6 (1-32) x AAV10887 (1-104)
 QY 1 LysTrpLysLeuPheLysLysLysLysLysLysLysLysLysLysLysValLeu 20
 DB 17 AATGGAAACTGTTCAAGAGATCGGCATCGCGCC-----GTGCTGAAGTGTG 67
 QY 21 ThrThrGlyLeuProAlaLeu 27
 DB 68 ACCACCGGTCTGCCGGCGCTG 88
 RESULT 6
 AAT33489/c
 ID AAT33489 standard; DNA; 112 BP.
 XX AAT33489;
 AC AAT33489;
 XX 21-MAY-1997 (first entry)
 DT 112mer encoding CEMA.
 DE Cationic peptide; CEMA; CEME; cecropia; melittin; bacterial growth;
 KW antibiotic activity; permeable; bacterial outer membrane;
 KW lipopolysaccharide; fusion peptide; inhibition; endotoxaemia;
 KW sepsis associated disorder; septic shock; ss.
 OS Synthetic.
 XX

PN WO9628559-A1.
 XX 19-SEP-1996.
 XX 13-MAR-1996; 96WO-IB000431.
 PF 13-MAR-1995; 95US-00405234.
 PR (UYBR-) UNIV BRITISH COLUMBIA.
 PA Hancock REW, Piers KL, Brown MH, Kelly N;
 PI WPI; 1996-433831/43.
 XX Recombinant production of antimicrobial, cationic peptide - produced in
 PT bacterial host as fusion peptide with an anionic portion for suppressing
 PT the anti-microbial activity of the cationic peptide.
 XX Example 2; Page 19; 90pp; English.
 PS The sequences given in AAT33488-500 and AAT40195-204 are oligonucleotides
 CC which were used in the construction of vectors used in the method of the
 CC invention. The method comprises constructing an expression vector
 CC containing DNA encoding the cationic peptide adjacent to DNA encoding an
 CC anionic carrier peptide which inhibits bacterial proteases. A bacterial
 CC host cell is transformed with the vector and cultured to express a fusion
 CC peptide comprising the cationic and anionic peptides. The biologically
 CC active cationic peptide is then recovered. The vectors constructed using
 CC these sequences encode CEME, CEMA or HNP-1 (human neutrophil peptide 1).
 CC CEMA contains the first 18 amino acids of cecropin A and the last 8
 CC residues of melittin. CEMA is derived from CEME by changing the C-
 CC terminal amino acid of CEME to include two additional Lys residues. This
 CC modification improves the antibiotic activity of the peptide against many
 CC bacterial species, two fold, as well as substantially enhancing its
 CC ability to permeabilise bacterial outer membranes and to bind to
 CC lipopolysaccharide. CEMA and CEME act to permeabilise bacterial membranes
 CC breaking down the outer membrane permeability barrier. They may be used
 CC in conjunction with antibiotics to inhibit bacterial growth and to treat
 CC an endotoxaemia or sepsis associated disorders e.g. septic shock
 XX Sequence 112 BP; 22 A; 33 C; 28 G; 29 T; 0 U; 0 Other;
 SQ Alignment Scores: 1.68e-09 Length: 112
 Pred. No.: 109.50 Matches: 24
 Score: 88.89% Conservative: 0
 Percent Similarity: 88.89% Mismatches: 0
 Best Local Similarity: 88.89% Indels: 3
 Query Match: 69.75% Gaps: 1
 DB: 2
 US-10-823-425-6 (1-32) x AAT33489 (1-112)
 QY 1 LysTrpLysLeuPheLysLysLysLysLysLysLysLysLysLysLysValLeu 20
 DB 92 AATGGAAACTGTTCAAGAGATCGGCATCGCGCC-----GTGCTGAAGTGTG 42
 QY 21 ThrThrGlyLeuProAlaLeu 27
 DB 41 ACCACCGGTCTGCCGGCGCTG 21
 RESULT 7
 AAT63052/c
 ID AAT63052 standard; DNA; 112 BP.
 XX AAT63052;
 AC AAT63052;
 XX 25-MAR-2003 (revised)
 DT 08-MAY-1997 (first entry)
 XX 112-mer encoding CEME.
 DE HNP-1; CEME; CEMA; human neutrophil protein; fusion; insect defensin;
 KW cecropin A; bee venom; melittin; antibiotic activity; S. typhimurium;
 KW

KW permeability; bacterial outer membrane; lipopolysaccharide; antibiotic;
 KW E. coli; Pseudomonas aeruginosa; E. cloacae; S. aureus; ss.

Synthetic.

XX US593866-A.

XX 14-JAN-1997.

XX 20-DEC-1995; 95US-00575052.

XX 21-AUG-1992; 92US-00933492.

XX 20-AUG-1993; 93US-00110502.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Brown MH, Piers KL, Hancock REW;

XX WPI; 1997-099468/09.

XX Prodn. of recombinant cationic peptide with antimicrobial activity - in

PT the form of a fusion peptide with protease-inhibiting anionic peptide.

XX Example 1; Col 9-10; 31pp; English.

XX The sequences given in AAT63051-64 represent oligonucleotides which were
 CC used in the construction of pGST-ppetide plasmids for the expression of
 CC HNP-1, CEME and CEMA. HNP-1 is peptide 1 from human neutrophil protein,
 CC CEME is a fusion peptide made from portions of an insect defensin
 CC cecropin A and the bee venom peptide melittin, and CEMA is a variant of
 CC CEME with two additional lysine residues at the C-terminal end. The
 CC modification from CEME to CEMA causes a two-fold improvement in
 CC antibiotic activity against many bacterial species as well as
 CC substantially enhancing the ability to permeabilise bacterial outer
 CC membranes and binding to lipopolysaccharides. CEMA may be used
 CC synergistically with classical antibiotics to break down the outer
 CC membrane permeability barrier. It is possibly active against E. coli,
 CC Pseudomonas aeruginosa, E. cloacae, S. typhimurium and S. aureus.
 CC (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 112 BP; 22 A; 33 C; 28 G; 29 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.68e-09 Length: 112
 Score: 109.50 Matches: 24
 Percent Similarity: 88.89% Conservative: 0
 Best Local Similarity: 88.89% Mismatches: 0
 Query Match: 69.75% Indels: 3
 DB: 2 Gaps: 1

US-10-823-425-6 (1-32) x AAT63052 (1-112)

QY 1 LysTrpLysLeuPheLysValleGlyIleGlyAlaValLeuLysValLeuLysValLeu 20
 Db 92 AATGGAAACTGTTCAAGAGATCGGCATCGGCGCC-----GTGCTGAAGTGTG 42

QY 21 ThrThrGlyLeuProAlaLeu 27

Db 41 ACCACCGGTCTGCGGCGCTG 21

RESULT 8

AAV10888/C

ID AAV10888 standard; DNA; 112 BP.

XX AAV10888;

XX 14-JUL-1998 (first entry)

XX Human cecropin A/melittin hybrid peptide primer 2.

KW Cecropin A; melittin; CEME; fusion protein; polycationic; antibacterial;
 KW permeable; outer membrane; lipopolysaccharide; bacterial infection;
 KW septic shock; primer; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX US5707855-A.

XX 13-JAN-1998.

XX 20-DEC-1996; 96US-00770557.

XX 21-AUG-1992; 92US-00933492.

XX 20-AUG-1993; 93US-00110502.

XX 20-DEC-1995; 95US-00575052.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Brown MH, Piers KL, Hancock REW;

XX WPI; 1998-100348/09.

XX Antibacterial peptide CEMA - useful for treating bacterial infections and

PT septic shock.

XX Example 1; Col 10; 31pp; English.

XX AAV10887-V10909 are primers used in a method which allows the production

CC of a novel polycationic antibacterial peptide, CEMA. This peptide is a is

CC a hybrid comprising the first 18 amino acids of cecropin A and the last 8

CC amino acids of melittin. It has two Lys residues at the C terminus which

CC creates a sequence with two-fold increased antibiotic activity against

CC many bacterial species as well as enhanced ability to permeabilise

CC bacterial outer membranes and bind to lipopolysaccharide. CEMA can be

CC used to treat bacterial infections and septic shock

XX Sequence 112 BP; 22 A; 33 C; 28 G; 29 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.68e-09 Length: 112
 Score: 109.50 Matches: 24
 Percent Similarity: 88.89% Conservative: 0
 Best Local Similarity: 88.89% Mismatches: 0
 Query Match: 69.75% Indels: 3
 DB: 2 Gaps: 1

US-10-823-425-6 (1-32) x AAV10888 (1-112)

QY 1 LysTrpLysLeuPheLysValleGlyIleGlyAlaValLeuLysValLeuLysValLeu 20

Db 92 AATGGAAACTGTTCAAGAGATCGGCATCGGCGCC-----GTGCTGAAGTGTG 42

QY 21 ThrThrGlyLeuProAlaLeu 27

Db 41 ACCACCGGTCTGCGGCGCTG 21

RESULT 9

ADM56051

ID ADM56051 standard; DNA; 78 BP.

XX ADM56051;

XX 03-JUN-2004 (first entry)

XX Antibacterial peptide GK-1 encoding DNA.

XX antibacterial peptide; bactericidal; antibacterial;

XX solid-phase chemical process; gene engineering expression;

XX Gram-negative bacterium; Gram-positive bacterium; fungal infection;

XX infection; gene; ds.

XX Synthetic.

XX Key Location/Qualifiers

FT 7. .78

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FT      /*tag= a
FT      /product= "CK-1"
PN      CN1398897-A.
XX      26-FEB-2003.
XX      XX
PF      02-SEP-2002; 2002CN-00136766.
XX      PD
XX      PR      02-SEP-2002; 2002CN-00136766.
XX      PA      (SHAN-) SHANGHAI GAOKE UNION BIOTECHNOLOGY DEV C.
XX      PI      Huang Q;
XX      XX
XX      WPI; 2003-457919/44.
XX      DR      P-PSDB; ADM56050.
XX      XX
PT      Serial synthetic antibacterial peptide.
XX      PS      Example 2; Page 10; 41pp; Chinese.
XX      CC      The present invention describes a group of synthetic antibacterial
XX      CC      peptides with bactericidal activity stronger than that of a natural
XX      CC      antibacterial peptide. The synthetic antibacterial peptide is prepared by
XX      CC      the solid-phase chemical process or gene engineering expression. The
XX      CC      synthetic antibacterial peptide may be used in preparing medicine for
XX      CC      treating diseases caused by Gram-negative bacterium, Gram-positive
XX      CC      bacterium and fungus infection. The present sequence encodes a peptide
XX      CC      from the present invention.
XX      SQ      Sequence 78 BP; 24 A; 17 C; 21 G; 16 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      0.00453      Length:      78
Score:          70.00      Matches:      13
Percent Similarity: 93.33%      Conservative: 1
Best Local Similarity: 86.67%      Mismatches: 1
Query Match:    44.59%      Indels:      0
DB:            11      Gaps:        0

US-10-823-425-6 (1-32) x ADM56051 (1-78)

QY      1 LysTrpLysLeuPhelysLysIleGlyIleGlyAlaValLeuLys 15
       7 AAATGGAACTGTTTAAAAAAATGGCAITGGCCGCTGCTGAAA 51

RESULT 10
ADM56057
ID      ADM56057 standard; DNA; 762 BP.
XX      AC      ADM56057;
XX      DT      03-JUN-2004 (first entry)
XX      DE      GST-GK-1 protein encoding DNA.
XX      KW      antibacterial peptide; bactericidal; antibacterial;
XX      KW      solid-phase chemical process; gene engineering expression;
XX      KW      Gram-negative bacterium; Gram-positive bacterium; fungal infection;
XX      KW      infection; GST; glutathione S transferase; gene; ds.
XX      OS      Synthetic.
XX      FH      Key      Location/Qualifiers
XX      FT      CDS      1..756
XX      FT      /*tag= a
XX      FT      /product= "GST-GK-1"
XX      PN      CN1398897-A.
XX      PD      26-FEB-2003.
XX      PT

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PF      02-SEP-2002; 2002CN-00136766.
XX      PR
XX      PR      02-SEP-2002; 2002CN-00136766.
XX      PA      (SHAN-) SHANGHAI GAOKE UNION BIOTECHNOLOGY DEV C.
XX      PI      Huang Q;
XX      XX
XX      WPI; 2003-457919/44.
XX      DR      P-PSDB; ADM56056.
XX      XX
PT      Serial synthetic antibacterial peptide.
XX      PS      Example 3; Page 12; 41pp; Chinese.
XX      CC      The present invention describes a group of synthetic antibacterial
XX      CC      peptides with bactericidal activity stronger than that of a natural
XX      CC      antibacterial peptide. The synthetic antibacterial peptide is prepared by
XX      CC      the solid-phase chemical process or gene engineering expression. The
XX      CC      synthetic antibacterial peptide may be used in preparing medicine for
XX      CC      treating diseases caused by Gram-negative bacterium, Gram-positive
XX      CC      bacterium and fungus infection. The present sequence encodes a GST-GK-1
XX      CC      protein, which is used in an example from the present invention.
XX      SQ      Sequence 762 BP; 242 A; 78 C; 129 G; 313 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      0.0869      Length:      762
Score:          70.00      Matches:      13
Percent Similarity: 93.33%      Conservative: 1
Best Local Similarity: 86.67%      Mismatches: 1
Query Match:    44.59%      Indels:      0
DB:            11      Gaps:        0

US-10-823-425-6 (1-32) x ADM56057 (1-762)

QY      1 LysTrpLysLeuPhelysLysIleGlyIleGlyAlaValLeuLys 15
       685 AAATGGAAATTTTAAAAAAATGGTATTGGTCGTTTAAAAA 729

RESULT 11
AAZ29391
ID      AAZ29391 standard; DNA; 48 BP.
XX      AC      AAZ29391;
XX      DT      29-FEB-2000 (first entry)
XX      DE      PCR primer-17 for synthesis of antimicrobial peptide Melittin gene.
XX      KW      PCR primer; anti-microbial peptide; Melittin gene; DNA construct;
XX      KW      glutamine pyrophosphoribosyl pyrophosphate amidotransferase gene;
XX      KW      purF gene; fusion peptide; mass production; pharmaceutical industry;
XX      KW      food industry; ss.
XX      OS      Synthetic.
XX      PN      WO9964611-A1.
XX      PD      16-DEC-1999.
XX      PP      08-JUN-1999; 99WO-KR000282.
XX      PR      09-JUN-1998; 98KR-00022117.
XX      PR      14-MAY-1999; 99KR-00017920.
XX      PA      (SAMY-) SAMYANG GENEX CORP.
XX      PI      Kim JH, Kang MH, Lee J, Park SH, Lee JW, Hong SS, Lee H;
XX      DR      WPI; 2000-097542/08.
XX      PT      New DNA constructs useful for mass production of antimicrobial peptides

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PT in microorganism hosts.

XX Example 1; Page 13; 67pp; English.

XX The present sequence is a chemically synthesised PCR primer which was used to synthesise a gene encoding antimicrobial peptide Melittin. The CC antimicrobial peptide gene is used in a DNA construct that comprises CC entire, partial or a derivative of purf gene (Glutamine CC pyrophosphoribosyl pyrophosphate amidotransferase gene). The DNA CC construct allows mass production of the antimicrobial peptide in CC microbial hosts without killing the host cells. The antimicrobial CC peptides are useful commercially in the pharmaceutical and food CC industries

XX Sequence 48 BP; 6 A; 13 C; 17 G; 12 T; 0 U; 0 Other;

Alignment Scores: 0.0203 Length: 48
Pred. No.: 64.50 Matches: 16
Score: 84.21% Conservative: 0
Percent Similarity: 84.21% Mismatches: 0
Best Local Similarity: 84.21% Indels: 3
Query Match: 41.08% Indels: 3
DB: 3 Gaps: 1

US-10-823-425-6 (1-32) x AAZ29391 (1-48)

QY 9 GlyIleGlyAlaValLeuLysValLeuLysValLeuThrGlyLeuProAlaLeu 27
Db 1 GGTATCGGTGCG-----GTTCTGAAAGTTCTGACCACCGGTCTGCGGCGCTG 48

RESULT 12

ABL60416

ID ABL60416 standard; DNA; 48 BP.

XX ABL60416;

DT 28-MAR-2003 (first entry)

DE DNA fragment of the invention #17.

XX Gene expression; peptide antibiotic; purf gene; ds.

XX Unidentified.

XX KR2001098973-A.

XX 08-NOV-2001.

XX 08-JUN-2001; 2001KR-00031889.

XX 08-JUN-2001; 2001KR-00031889.

XX (SAMY-) SAMYANG GENEX CORP.

PI Hong SS, Kang MH, Kim JH, Lee HS, Lee JH, Lee JW, Park SH;

DR WPI; 2002-301977/34.

XX Gene expression system useful for mass-production of peptide antibiotics and vectors derived from microorganisms.

XX Disclosure; Page 7; 56pp; Korean.

XX The invention relates to a genetic component which mass-produces peptide antibiotics effectively from microorganisms. The genetic component consists of a first gene sequence which codes for the whole or partial purf gene or its derivative, and a second gene sequence which codes peptide antibiotics. The mass-production method of peptide antibiotics comprises the steps of: constructing an expression vector including the genetic component, transforming a bacterial host cell with the vector, culturing the transformed cell to express the genetic component, and recovering the peptide antibiotics. The expression vector is selected from the group consisting of pGNX2, pGNX3, pGNX4 and pGNX5, and it has a

CC high copy number of origin, strong transcription promoter and structural gene. The sequences given in records ABL60400-ABL60464 represent DNA CC sequences of the invention

XX Sequence 48 BP; 6 A; 13 C; 17 G; 12 T; 0 U; 0 Other;

Alignment Scores: 0.0203 Length: 48
Pred. No.: 64.50 Matches: 16
Score: 84.21% Conservative: 0
Percent Similarity: 84.21% Mismatches: 0
Best Local Similarity: 84.21% Indels: 3
Query Match: 41.08% Indels: 3
DB: 6 Gaps: 1

US-10-823-425-6 (1-32) x ABL60416 (1-48)

QY 9 GlyIleGlyAlaValLeuLysValLeuLysValLeuThrGlyLeuProAlaLeu 27
Db 1 GGTATCGGTGCG-----GTTCTGAAAGTTCTGACCACCGGTCTGCGGCGCTG 48

RESULT 13

AAL56635

ID AAL56635 standard; cDNA; 213 BP.

XX AAL56635;

DT 25-SEP-2003 (first entry)

DE cDNA encoding the bee and hornet peptide precursor prepromelittin.

XX Bee; hornet; aptoxin haemolysis; prepromelittin; pesticide; antibody; ss; Gene.

XX Apis mellifera.

XX Key Location/Qualifiers

FT CDS 1..213

FT /tag= a

FT /product= "Promelittin protein"

XX CN1377964-A.

XX 06-NOV-2002.

XX 01-FEB-2002; 2002CN-00110748.

XX 01-FEB-2002; 2002CN-00110748.

XX (UYZH-) UNIV ZHEJIANG.

XX Shi W, Zhang C, Zhang S;

XX WPI; 2003-211617/21.

XX P-PSDB; AA023288.

XX China bee and hornet hemolysis peptide precursor gene, its encoded polypeptide, and preparation method.

XX Claim 1; Page 14; 15pp; Chinese.

XX This invention relates to a novel Chinese bee and hornet aptoxin haemolysis peptide precursor, prepromelittin. This protein can be used as a diagnosis reagent, biochemical reagent and a biological pesticide, as well as for further research purposes. In addition, the present invention also describes the polynucleotide encoding the prepromelittin, its production and a relevant antibody. This polynucleotide sequence is the Chinese bee and hornet prepromelittin cDNA of the invention

XX Sequence 213 BP; 58 A; 45 C; 58 G; 52 T; 0 U; 0 Other;

Alignment Scores: 0.14 Length: 213
Pred. No.: 64.50 Matches: 16

Percent Similarity: 84.21% Conservative: 0
 Best Local Similarity: 84.21% Mismatches: 0
 Query Match: 41.08% Indels: 3
 DB: 10 Gaps: 1

US-10-823-425-6 (1-32) x AAL56635 (1-213)

QY 9 GlyIleGlyAlaValLeuLysValLeuThrThrGlyLeuProAlaLeu 27
 |||||
 Db 130 GGAATTGGAGCA-----GTTCTCAAAGTATTAAACCACAGGATTGCTGCCCTT 177

RESULT 14

ADL06283
 ID ADL06283 standard; cDNA; 213 BP.
 AC ADL06283;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE cDNA encoding ink chest wasp venom haemolytic peptide precursor.
 XX
 KW Ink chest wasp venom haemolytic peptide precursor; italian bee venom;
 KW Gene; ss.
 XX
 OS Insecta.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..213
 FT /*tag= a
 FT /product= "Haemolytic peptide precursor"

XX CN1385526-A.

XX 18-DEC-2002.

XX 01-FEB-2002; 2002CN-00110751.

XX 01-FEB-2002; 2002CN-00110751.

XX (UYZK-) UNIV ZHEJIANG.

XX Shi W, Zhang C, Zhang S;

XX WPI; 2003-301690/30.

XX P-PSDB; ADL06284.

XX Precursor gene of ink chest wasp aptoxin bematolysis peptide, its coded polypeptide and preparation process thereof.

XX Claim 1; SEQ ID NO 5; 15pp; Chinese.

XX The present invention relates to a coding sequence for ink chest wasp venom haemolytic peptide precursor gene, and the polypeptide it encodes. The ink chest wasp venom haemolytic peptide precursor is a homologue of Italian bee venom haemolytic peptide precursor. Also disclosed is a preparation method of a vector containing the polynucleotide sequence encoding ink chest wasp venom haemolytic peptide precursor, a host cell containing the vector, and an antibody related to the ink chest wasp venom haemolytic peptide precursor. The present sequence encodes ink chest wasp venom haemolytic peptide precursor.

SQ Sequence 213 BP; 59 A; 45 C; 57 G; 52 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0.14 Length: 213
 Score: 64.50 Matches: 16
 Percent Similarity: 84.21% Conservative: 0
 Best Local Similarity: 84.21% Mismatches: 0
 Query Match: 41.08% Indels: 3
 DB: 10 Gaps: 1

US-10-823-425-6 (1-32) x ADL06283 (1-213)

QY 9 GlyIleGlyAlaValLeuLysValLeuThrThrGlyLeuProAlaLeu 27
 |||||
 Db 130 GGAATTGGAGCA-----GTTCTCAAAGTATTAAACCACAGGATTGCTGCCCTT 177

RESULT 15

ADB69787
 ID ADB69787 standard; DNA; 1245 BP.

AC ADB69787;

XX 04-DEC-2003 (first entry)

XX C. neoformans open reading frame SEQ ID NO:2192.

XX ds; gene; fungicide; gene therapy; infection.

XX Cryptococcus neoformans.

XX WO2003052076-A2.

XX 26-JUN-2003.

XX 17-DEC-2002; 2002WO-US040225.

XX 17-DEC-2001; 2001US-0341261P.

XX (ELIT-) ELITRA PHARM INC.

XX Zamudio C, Eroshkin AM;

XX WPI; 2003-533017/50.

XX P-PSDB; ADB70148.

XX New nucleic acid, useful for preparing a composition for treating an infection caused by Cryptococcus neoformans.

XX Claim 2; SEQ ID NO 2192; 136pp; English.

XX The invention relates to a novel purified or isolated Cryptococcus neoformans nucleic acid molecule comprising a sequence encoding a polypeptide comprising a sequence not given in the specification. A polynucleotide of the invention has fungicide activity, and may have a use in gene therapy. The nucleic acid is useful for preparing a composition for treating an infection caused by Cryptococcus neoformans. The present sequence represents a C. neoformans sequence of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX SQ Sequence 1245 BP; 314 A; 275 C; 298 G; 358 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.67 Length: 1245
 Score: 64.00 Matches: 17
 Percent Similarity: 61.29% Conservative: 2
 Best Local Similarity: 54.84% Mismatches: 11
 Query Match: 40.76% Indels: 1
 DB: 10 Gaps: 0

US-10-823-425-6 (1-32) x ADB69787 (1-1245)

QY 2 TrpLysLeuPhelysLysIleGlyIleGlyAlaValLeuLysValLeu-LysValLeuTh 21
 |||||
 Db 1042 TGGGGTAAACTTCAAGTCTCTGTATCGGAACAGCTTTGAGATCCTTTTGAGCTTGAC 1101
 QY 21 rThrGlyLeuProAlaLeuLysLeuThrLeu 31
 |||||
 Db 1102 GACAGGGCTCTCGACCCCTAAAGTTAACCTG 1132

Search completed: January 15, 2006, 18:51:20
 Job time : 518 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 18:05:08 ; Search time 3789 Seconds
(without alignments)
395.140 Million cell updates/sec

Title: US-10-823-425-6
Perfect score: 157
Sequence: 1 KKKLPKIGIGAVLVKLVLTGLPALKLTLLK 32

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlp
-O=/cgn2.1/USPTO.spool.p/US10823425/runat.13012006.095447.27894/app.query.fasta_1.199
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNIT8=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10823425 @CGN 1.1 8010 @runat.13012006.095447.27894 -NCPU=6
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPHLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hcc1:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	64	40.8	492	6	CF712874 CCAB147F
C 2	64	40.8	768	6	CF700264 CCACQ86TF
C 3	64	40.8	781	6	CF699580 CCAH947TF
C 4	64	40.8	797	6	CF714188 CCAG087TF
C 5	64	40.8	799	6	CF675888 CCAB105TF
C 6	64	40.8	887	6	CF708880 CCAGJ94TF
C 7	62	39.5	767	9	BZ620354 1g44a07.g

C	8	62	39.5	793	10	CG437027
C	9	62	39.5	821	10	CG437034
C	10	62	39.5	852	9	CC623929
C	11	62	39.5	903	10	CG242180
C	12	62	39.5	939	10	CG268790
C	13	60.5	38.5	586	9	BZ299309
C	14	60	38.2	1119	9	CG243842
C	15	58.5	37.3	383	1	AA746677
C	16	58.5	37.3	949	10	CNS026CP
C	17	58	36.9	329	8	R81054
C	18	58	36.9	741	8	DN227874
C	19	58	36.9	799	6	CD437473
C	20	58	36.9	812	9	AZ535158
C	21	58	36.9	838	9	AZ675038
C	22	58	36.9	840	9	AZ535161
C	23	58	36.9	841	9	AZ686443
C	24	58	36.9	849	9	AZ686667
C	25	58	36.9	873	9	AZ528338
C	26	58	36.9	904	9	BH152353
C	27	58	36.9	918	10	CG108626
C	28	58	36.9	930	10	CG108625
C	29	57.5	36.6	580	9	B89915
C	30	57	36.3	335	1	AW432138
C	31	57	36.3	648	1	AV610115
C	32	57	36.3	690	7	CK722149
C	33	57	36.3	736	10	AG558427
C	34	57	36.3	781	7	CK770581
C	35	57	36.3	845	1	AM015780
C	36	56.5	36.0	460	7	CO724350
C	37	56.5	36.0	556	5	BY603938
C	38	56.5	36.0	809	2	B1248983
C	39	56.5	36.0	829	10	CG112422
C	40	56.5	36.0	971	6	CF241970
C	41	56	35.7	324	2	BB500449
C	42	56	35.7	483	6	CB063360
C	43	56	35.7	596	1	AW596420
C	44	56	35.7	642	11	DE110442
C	45	56	35.7	656	6	CF788205

ALIGNMENTS

RESULT 1
CF712874/c

LOCUS CF712874 492 bp mRNA linear EST 16-AUG-2004
DEFINITION CCAB147F C.neoformans strain JEC21 Cryptococcus neoformans var.
ACCESSION CF712874
VERSION CF712874.1 GI:41567033
KEYWORDS EST.
SOURCE Cryptococcus neoformans var. neoformans (Filobasidiella neoformans var. neoformans)
ORGANISM Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE 1 (bases 1 to 492)
AUTHORS Loftus,B.
TITLE End sequencing of clones from a Full length enriched, normalized JEC21 cDNA library
JOURNAL Unpublished (2003)
COMMENT Other ESTs: CCAB147R
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: b.loftus@tigr.org
Seq primer: TF.

FEATURES
source
1..492
/mol_type="mRNA"
/organism="Cryptococcus neoformans var. neoformans"
Location/Qualifiers

CF788205 856965 MA

```

/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAB14"
/clone_lib="C.neoformans strain JEC21"
/note="Vector: pCMVSPORT6; Site 1: NotI EcorV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

```

ORIGIN

```

Alignment Scores:
Pred. No.: 9.91 Length: 492
Score: 64.00 Matches: 17
Percent Similarity: 61.29% Conservative: 2
Best Local Similarity: 54.84% Mismatches: 11
Query Match: 40.76% Indels: 1
DB: 6 Gaps: 0

```

US-10-823-425-6 (1-32) x CF712874 (1-492)

```

QY 2 TrpLysLeuPheLysLysLleGlyAlaValLeuLysValLeu-LysValLeuTh 21
   |||
   ::|
Db 471 TGGGGTAAACTTCAAGTCTCTGATCGAACACAGCTTTGAAGATCCTTTTGAGCTTGAC 412
QY 21 rThrGlyLeuProAlaLeuLysLeuThrLeu 31
   |||
   ::|
Db 411 GACAGGGCTCTCGACCCCTAAAGTTAACCCCTG 381

```

RESULT 2

```

CF700264/c
LOCUS CF700264 768 bp mRNA linear EST 16-AUG-2004
DEFINITION CCAQ86TF C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAQ86, mRNA sequence.

```

```

ACCESSION CF700264.1 GI:41554423
VERSION
KEYWORDS
SOURCE
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)

```

```

ORGANISM
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

```

REFERENCE 1 (bases 1 to 768)

```

AUTHORS Loftus,B.
TITLE End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: CCAQ86TR
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TF.

```

FEATURES

```

source
1..768
Location/Qualifiers
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAQ86"
/note="Vector: pCMVSPORT6; Site 1: NotI EcorV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

```

ORIGIN

```

Alignment Scores:
Pred. No.: 17.3 Length: 768
Score: 64.00 Matches: 17
Percent Similarity: 61.29% Conservative: 2

```

```

Best Local Similarity: 54.84% Mismatches: 11
Query Match: 40.76% Indels: 1
DB: 6 Gaps: 0

```

US-10-823-425-6 (1-32) x CF700264 (1-768)

```

QY 2 TrpLysLeuPheLysLysLleGlyAlaValLeuLysValLeu-LysValLeuTh 21
   |||
   ::|
Db 473 TGGGGTAAACTTCAAGTCTCTGATCGAACACAGCTTTGAAGATCCTTTTGAGCTTGAC 414
QY 21 rThrGlyLeuProAlaLeuLysLeuThrLeu 31
   |||
   ::|
Db 413 GACAGGGCTCTCGACCCCTAAAGTTAACCCCTG 383

```

RESULT 3

```

CF699580/c
LOCUS CF699580 781 bp mRNA linear EST 16-AUG-2004
DEFINITION CCAH947TF C.neoformans strain JEC21 Cryptococcus neoformans var.
neoformans cDNA clone CCAH947, mRNA sequence.

```

```

ACCESSION CF699580.1 GI:41553739
VERSION
KEYWORDS
SOURCE
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)

```

```

ORGANISM
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

```

REFERENCE 1 (bases 1 to 781)

```

AUTHORS Loftus,B.
TITLE End sequencing of clones from a Full length enriched, normalized
JEC21 cDNA library
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: CCAH947TR
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: bjloftus@tigr.org
Seq primer: TF.

```

FEATURES

```

source
1..781
Location/Qualifiers
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCA947"
/note="Vector: pCMVSPORT6; Site 1: NotI EcorV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

```

ORIGIN

```

Alignment Scores:
Pred. No.: 17.7 Length: 781
Score: 64.00 Matches: 17
Percent Similarity: 61.29% Conservative: 2
Best Local Similarity: 54.84% Mismatches: 11
Query Match: 40.76% Indels: 1
DB: 6 Gaps: 0

```

US-10-823-425-6 (1-32) x CF699580 (1-781)

```

QY 2 TrpLysLeuPheLysLysLleGlyAlaValLeuLysValLeu-LysValLeuTh 21
   |||
   ::|
Db 424 TGGGGTAAACTTCAAGTCTCTGATCGAACACAGCTTTGAAGATCCTTTTGAGCTTGAC 365
QY 21 rThrGlyLeuProAlaLeuLysLeuThrLeu 31
   |||
   ::|
Db 364 GACAGGGCTCTCGACCCCTAAAGTTAACCCCTG 334

```



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source
1. 887
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="JEC21"
/db_xref="taxon:40410"
/clone="CCAG194"
/clone_lib="C.neoformans strain JEC21"
/notes="Vector: pCWSPORT6; Site 1: NotI-EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Alignment Scores:
Pred. No.: 20.8 Length: 887
Score: 64.00 Matches: 17
Percent Similarity: 61.24% Conservative: 2
Best Local Similarity: 54.84% Mismatches: 11
Query Match: 40.76% Indels: 1
DB: 6 Gaps: 0

US-10-823-425-6 (1-32) x CF708880 (1-887)

QY 2 TtpLysLeuPhelLysLysileGlyAlaValLeuLysValLeu-LysValLeuTh 21
Db 490 TGGGGTAAACTCAAGTCCTCGTATCGGACAGCTTTGAGATCCTTTTGAGCTTGAC 431

QY 21 rThrGlyLeuProAlaLeuLysLeuThrLeu 31
Db 430 GACAGGGCTCTCGACCCATAAGTTAACCCCTG 400

RESULT 7
BZ620354/c
LOCUS
DEFINITION
BZ620354 767 bp DNA linear GSS 16-JAN-2003
ig44a07.g1 WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone
ig44a07.5', genomic survey sequence.
ACCESSION
BZ620354
VERSION
BZ620354.1 GI:27772206
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 767)
Rabinowicz,P.D., O'Shaughnessy,A.L., Ballija,V., Dedhia,N.,
Katzburger,F., King,L., Miller,B., Muller,S., Nascimeto,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100 Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: ig44 row: a column: 07
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence stop: 767.
Location/Qualifiers
1. 767
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ig44a07"
/lab_host="DH5a"
/notes="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
source

FEATURES
source
1. 767
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM0847003"
/clone_lib="ZM 0.7 1.5 KB"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Alignment Scores:
Pred. No.: 37.8 Length: 793
Score: 62.00 Matches: 13
Percent Similarity: 70.83% Conservative: 4
Best Local Similarity: 54.17% Mismatches: 7
Query Match: 39.49% Indels: 0
DB: 10 Gaps: 0

US-10-823-425-6 (1-32) x BZ620354 (1-767)

QY 8 lleGlyileGlyAlaValLeuLysValLeuThrThrGlyLeuProAlaLeu 27
Db 87 ATAGGGGTAGGGCGCTAGCTGCACGCTGTGTGAATCTTGGCGCGTGTCCGCTGTC 28

QY 28 LysLeuThrLeu 31
Db 27 AAGCTGACTCTG 16

RESULT 8
CG437027/c
LOCUS
DEFINITION
CG437027 793 bp DNA linear GSS 17-SEP-2003
CG7AI86TH ZM 0.7_1.5_KB Zea mays genomic clone ZM0847003,
genomic survey sequence.
ACCESSION
CG437027
VERSION
CG437027.1 GI:34813566
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 793)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: CG7AI86TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
1. 793
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM0847003"
/clone_lib="ZM 0.7 1.5 KB"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Alignment Scores:
Pred. No.: 37.8 Length: 793
Score: 62.00 Matches: 13
Percent Similarity: 70.83% Conservative: 4
Best Local Similarity: 54.17% Mismatches: 7
Query Match: 39.49% Indels: 0
DB: 10 Gaps: 0

was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector (.x/y
reads in M13mpl9, .b/g reads in pUC19). The same ligation
was transformed into DH5a."

```



```

Db      163 AATCTGAAGATTGGTCCAGACGAACATGTTGAAGACTCTTTCCAATGGCTTACCGTCA 222
          :::::||||| |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Qy      27 LeuLysLeuThrLeu 31
          ::: :::::||||
Db      223 GTGTCGGTTTCCTTG 237
          ::: :::::||||

RESULT 14
CC243842
LOCUS   CC243842
DEFINITION CH261-12G9 Sp6.1 CH261 Gallus gallus genomic clone CH261-12G9,
          genomic survey sequence.
ACCESSION CC243842
VERSION   CC243842.1 GI:30570505
KEYWORDS GSS.
SOURCE   CC243842.1
ORGANISM Gallus gallus (chicken)
          Gallus gallus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
          Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1119)
AUTHORS   Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,
          Warren,W., Graves,T., Mardis,B. and Wilson,R.
TITLE     Gallus gallus BAC End Reads
JOURNAL   Unpublished (2003)
COMMENT   Contact: Richard K. Wilson
          Genome Sequencing Center
          Washington University School of Medicine
          Email: submissions@watson.wustl.edu
          Insert Length: 182000 Std Error: 0.00
          Seg primer: Sp6 ATTAGGTGACACTATAG
          Class: BAC ends
          High quality sequence start: 32
          High quality sequence stop: 787.

FEATURES             source
     source          1..1119
     /organism="Gallus gallus"
     /mol_type="genomic DNA"
     /strain="Red Jungle Fowl"
     /db_xref="taxon:9031"
     /clone="CH261-12G9"
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     /cell_line="UCD001, inbred 256"
     /clone_lib="CH261"
     /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
     CH261 Female Chicken library - For library and clone
     ordering information: http://www.chori.org/bacpac"

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Score:          60.00      Matches:      14
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Best Local Similarity: 45.16%      Mismatches: 13
Query Match:     38.22%      Indels: 0
DB:              9      Gaps: 0

US-10-823-425-6 (1-32) x CC243842 (1-1119)

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Qy      22 ThrGlyLeuProAlaLeuLysLeuThrLeuLys 32
          ||| :::::||||| ::::: |||||
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LOCUS   AA746677
DEFINITION nx62b10.s1 NCI CGAP Alvl Homo sapiens cDNA clone IMAGE:1266811
          similar to gp:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);, mRNA
          sequence.

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 18:54:08 ; Search time 148 Seconds
(without alignments)
384.338 Million cell updates/sec

Title: US-10-823-425-6
Perfect score: 157
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	109.5	69.7	104	2	US-08-770-557-1
4	109.5	69.7	104	2	US-08-405-234-1
C 5	109.5	69.7	112	2	US-08-575-052-2
C 6	109.5	69.7	112	2	US-08-614-516A-2
C 7	109.5	69.7	112	2	US-08-770-557-2
C 8	109.5	69.7	112	2	US-08-405-234-2
9	64.5	41.1	48	3	US-09-485-147A-17

10	64.5	41.1	88	3	US-09-485-147A-53	Sequence 53, Appl
11	59.5	37.9	78	3	US-09-230-180-33	Sequence 33, Appl
12	56.5	36.0	83349	3	US-09-949-016-17149	Sequence 17149, A
C 13	56	35.7	601	3	US-09-949-016-175049	Sequence 175049,
C 14	56	35.7	601	3	US-09-949-016-175050	Sequence 175050,
15	56	35.7	5871	3	US-10-152-886-24	Sequence 24, Appl
16	56	35.7	30922	3	US-09-949-016-16700	Sequence 16700, A
17	55	35.0	601	3	US-09-949-016-188989	Sequence 188989, A
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21	53.5	34.1	4411529	3	US-09-103-840A-1	Sequence 1, Appl
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27	52.5	33.4	1947	3	US-10-020-079-11	Sequence 11, Appl
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29	52.5	33.4	1965	3	US-10-020-079-9	Sequence 9, Appl
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32	52.5	33.4	2256	3	US-10-413-437-7	Sequence 7, Appl
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43	52.5	33.4	2592	3	US-10-020-079-31	Sequence 31, Appl
44	52.5	33.4	2592	3	US-10-413-437-31	Sequence 31, Appl
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ALIGNMENTS

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US-08-575-052-1
; Sequence 1, Application US/08575052
; Patent No. 5593866
; GENERAL INFORMATION:
; APPLICANT: HANCOCK, ROBERT E.W.
; APPLICANT: PIERS, KEVIN L.
; APPLICANT: BROWN, MELISSA H.
; TITLE OF INVENTION: CATIONIC PEPTIDES AND METHOD FOR PRODUCTION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JURAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 90067
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,052
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,502
; FILING DATE: 20-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR., PH.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD2823

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; TELECOMMUNICATION INFORMATION:
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; TELEFAX: 619/455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..104
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Score: 109.50 Matches: 24
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Query Match: 69.75% Indels: 3
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Qy 1 LysTrpLysLeuPheLysValIleGlyAlaValLeuLysValLeu 20
Db 17 AAATGGAAACTGTTCAAGAGATCGGCATCGCGCC-----GTGCTGAAGTGCTG 67
Qy 21 ThrThrGlyLeuProAlaLeu 27
Db 68 ACCACCGGCTGCGCGGCTG 88
RESULT 2
US-08-614-516A-1
; Sequence 1, Application US/08614516A
; Patent No. 5688767
; GENERAL INFORMATION:
; APPLICANT: HANCOCK, ROBERT E.W.
; APPLICANT: PIERS, KEVIN L.
; APPLICANT: BROWN, MELISSA H.
; APPLICANT: KELLY, NIAMH
; TITLE OF INVENTION: TREATMENT OF ENDOTOXIN-ASSOCIATED
; DISORDERS WITH CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Ste. 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/614,516A
; FILING DATE: 13-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILE, PH.D., LISA A.
; REGISTRATION NUMBER: 36,347
; REFERENCE/DOCKET NUMBER: 07420/010001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; NAME/KEY: CDS
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Db 68 ACCACCGGCTGCGCGGCTG 88
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; Sequence 1, Application US/08770557
; Patent No. 5707855
; GENERAL INFORMATION:
; APPLICANT: HANCOCK, ROBERT E.W.
; APPLICANT: PIERS, KEVIN L.
; APPLICANT: BROWN, MELISSA H.
; TITLE OF INVENTION: CATIONIC PEPTIDES AND METHOD FOR PRODUCTION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 90067
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; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,052
; FILING DATE:
; APPLICATION NUMBER: US/08/110,502
; FILING DATE: 20-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR., PH.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD2823
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619/455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; NAME/KEY: CDS
; LOCATION: 2..104
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QY 21 ThrThrGlyLeuProAlaLeu 27
Db 41 ACCACCGGTCTGCCGCGCTG 21

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; Sequence 2, Application US/08614516A
; Patent No. 568767
; GENERAL INFORMATION:
; APPLICANT: HANCOCK, ROBERT E.W.
; APPLICANT: PIERS, KEVIN L.
; APPLICANT: BROWN, MELISSA H.
; APPLICANT: KELLY, NIAMH
; TITLE OF INVENTION: TREATMENT OF ENDOTOXIN-ASSOCIATED
; TITLE OF INVENTION: DISORDERS WITH CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Ste. 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/614,516A
; FILING DATE: 13-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILE, PH.D., LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/010001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..112
US-08-614-516A-2

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Query Match: 69.75% Indels: 3
DB: 2 Gaps: 1

US-10-823-425-6 (1-32) x US-08-614-516A-2 (1-112)

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QY 21 ThrThrGlyLeuProAlaLeu 27
Db 41 ACCACCGGTCTGCCGCGCTG 21

RESULT 7
US-08-770-557-2/c
; Sequence 2, Application US/08770557

; Patent No. 5707855
; GENERAL INFORMATION:
; APPLICANT: HANCOCK, ROBERT E.W.
; APPLICANT: PIERS, KEVIN L.
; APPLICANT: BROWN, MELISSA H.
; TITLE OF INVENTION: CATIONIC PEPTIDES AND METHOD FOR PRODUCTION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,557
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,052
; FILING DATE:
; APPLICATION NUMBER: US/08/110,502
; FILING DATE: 20-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR., PH.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD2823
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619/455-5110
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..112
US-08-770-557-2

Alignment Scores:
Pred. No.: 2,21e-10 Length: 112
Score: 109.50 Matches: 24
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 69.75% Indels: 3
DB: 2 Gaps: 1

US-10-823-425-6 (1-32) x US-08-770-557-2 (1-112)

QY 1 LysTrpLysLeuPheLysLysIleGlyIleGlyAlaValLeuLysValLeu 20
Db 92 AAATGGAACACTGTTCAAGAGATCGGCATCGGCGCC-----GTGCTGAAAGTGCTG 42

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Db 41 ACCACCGGTCTGCCGCGCTG 21

RESULT 8
US-08-405-234-2/c
; Sequence 2, Application US/08405234
; Patent No. 5789377
; GENERAL INFORMATION:
; APPLICANT: HANCOCK, ROBERT E.W.
; APPLICANT: PIERS, KEVIN L.
; APPLICANT: BROWN, MELISSA H.

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; APPLICANT: KELLY, NIAWH
; TITLE OF INVENTION: TREATMENT OF ENDOTOXIN-ASSOCIATED DISORDERS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,234
; FILING DATE: 13-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILLE, PH.D., LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: PD3535
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619/455-5110
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..112
; US-08-405-234-2

Alignment Scores:
Pred. No.: 2,21e-10 Length: 112
Score: 109.50 Matches: 24
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 69.75% Indels: 3
DB: 2 Gaps: 1

US-10-823-425-6 (1-32) x US-08-405-234-2 (1-112)

QY 1 LysTrpLysLeuPheLysLysIleGlyIleGlyAlaValLeuLysValLeuLysValLeu 20
Db 92 AAATGGAACCTGTTCAAGAAGATCGGCATCGCGCC-----GTGCTGAAGTGCTG 42
QY 21 ThrThrGlyLeuProLalaLeu 27
Db 41 ACCACCGGTCTGCCGCGCTG 21

RESULT 9
US-09-485-147A-17
; Sequence 17, Application US/09485147A
; Patent No. 6699689
; GENERAL INFORMATION:
; APPLICANT: SAMYANG GENEX CORPORATION
; TITLE OF INVENTION: MASS PRODUCTION METHOD OF ANTIMICROBIAL PEPTIDE AND DNA CONSTRUCT
; TITLE OF INVENTION: AND EXPRESSION SYSTEM THEREOF
; FILE REFERENCE: PA/SYG/00086
; CURRENT FILING DATE: 2000-04-25
; PRIOR FILING DATE: 1998-09-06
; PRIOR APPLICATION NUMBER: KR 1999-17920
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 93

US-10-823-425-6 (1-32) x US-09-485-147A-17 (1-48)

QY 9 GlyIleGlyAlaValLeuLysValLeuLysValLeuThrThrGlyLeuProLalaLeu 27
Db 1 GGTATCGGTGCG-----GTTCTGAAGTTCTGACCACCGGTCTGCCGCGCTG 48

RESULT 10
US-09-485-147A-53
; Sequence 53, Application US/09485147A
; Patent No. 6699689
; GENERAL INFORMATION:
; APPLICANT: SAMYANG GENEX CORPORATION
; TITLE OF INVENTION: MASS PRODUCTION METHOD OF ANTIMICROBIAL PEPTIDE AND DNA CONSTRUCT
; TITLE OF INVENTION: AND EXPRESSION SYSTEM THEREOF
; FILE REFERENCE: PA/SYG/00086
; CURRENT APPLICATION NUMBER: US/09/485,147A
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: KR 1998-22117
; PRIOR FILING DATE: 1998-09-06
; PRIOR APPLICATION NUMBER: KR 1999-17920
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: KopatentIn 1.71
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MELITTIN gene
; US-09-485-147A-53

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RESULT 11
US-09-230-180-33
; Sequence 33, Application US/09230180
; Patent No. 6183992
; GENERAL INFORMATION:
; APPLICANT: Kim, Sun-Chang
; APPLICANT: Lee, Jae Hyun
; APPLICANT: Kang, Min Hyung
; APPLICANT: Kim, Jeong Hyun
; APPLICANT: Hong, Seung-Sun
; APPLICANT: Lee, Hyun-Soo
```

```
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 17
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for the synthesis of Melittin (48mer)
; US-09-485-147A-17

Alignment Scores:
Pred. No.: 0.00366 Length: 48
Score: 64.50 Matches: 16
Percent Similarity: 84.21% Conservative: 0
Best Local Similarity: 84.21% Mismatches: 0
Query Match: 41.08% Indels: 3
DB: 3 Gaps: 1

US-10-823-425-6 (1-32) x US-09-485-147A-17 (1-48)

QY 9 GlyIleGlyAlaValLeuLysValLeuLysValLeuThrThrGlyLeuProLalaLeu 27
Db 1 GGTATCGGTGCG-----GTTCTGAAGTTCTGACCACCGGTCTGCCGCGCTG 48

RESULT 10
US-09-485-147A-53
; Sequence 53, Application US/09485147A
; Patent No. 6699689
; GENERAL INFORMATION:
; APPLICANT: SAMYANG GENEX CORPORATION
; TITLE OF INVENTION: MASS PRODUCTION METHOD OF ANTIMICROBIAL PEPTIDE AND DNA CONSTRUCT
; TITLE OF INVENTION: AND EXPRESSION SYSTEM THEREOF
; FILE REFERENCE: PA/SYG/00086
; CURRENT APPLICATION NUMBER: US/09/485,147A
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: KR 1998-22117
; PRIOR FILING DATE: 1998-09-06
; PRIOR APPLICATION NUMBER: KR 1999-17920
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 53
; LENGTH: 88
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MELITTIN gene
; US-09-485-147A-53

Alignment Scores:
Pred. No.: 0.00804 Length: 88
Score: 64.50 Matches: 16
Percent Similarity: 84.21% Conservative: 0
Best Local Similarity: 84.21% Mismatches: 0
Query Match: 41.08% Indels: 3
DB: 3 Gaps: 1

US-10-823-425-6 (1-32) x US-09-485-147A-53 (1-88)

QY 9 GlyIleGlyAlaValLeuLysValLeuLysValLeuThrThrGlyLeuProLalaLeu 27
Db 1 GGTATCGGTGCG-----GTTCTGAAGTTCTGACCACCGGTCTGCCGCGCTG 48

RESULT 11
US-09-230-180-33
; Sequence 33, Application US/09230180
; Patent No. 6183992
; GENERAL INFORMATION:
; APPLICANT: Kim, Sun-Chang
; APPLICANT: Lee, Jae Hyun
; APPLICANT: Kang, Min Hyung
; APPLICANT: Kim, Jeong Hyun
; APPLICANT: Hong, Seung-Sun
; APPLICANT: Lee, Hyun-Soo
```

APPLICANT: Samyang Genex Corporation
APPLICANT: Korea Advanced Institute of Science and Technology
TITLE OF INVENTION: METHOD FOR MASS PRODUCTION OF
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE
FILE REFERENCE: 6181/0F135
CURRENT APPLICATION NUMBER: US/09/230,180
CURRENT FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: PCT/KR98/00132
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: KR 13372/1998
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: KR 21312/1997
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 78
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA sequence deduced from Melittin peptide
OTHER INFORMATION: sequence based on codon usage of E. coli
US-09-230-180-33

Alignment Scores:
Pred. No.: 0.0493 Length: 78
Score: 59.50 Matches: 15
Percent Similarity: 78.95% Conservative: 0
Best Local Similarity: 78.95% Mismatches: 1
Query Match: 37.90% Indels: 3
DB: Gaps: 1

US-10-823-425-6 (1-32) x US-09-230-180-33 (1-78)

QY 9 GlyIleGlyAlaValLeuLysValLeuLysValLeuThrThrGlyLeuProAlaLeu 27
Db 1 GGTACTGGTGGG-----GTTCTGAAAGTTCTGACCACCGGTCTGCGCGGCGTG 48

RESULT 12
US-09-949-016-17149
Sequence 17149, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17149
LENGTH: 83349
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(83349)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17149

Alignment Scores:
Pred. No.: 1.35e+03 Length: 83349
Score: 56.50 Matches: 12
Percent Similarity: 67.86% Conservative: 7
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 35.99% Indels: 3

DB: 3 Gaps: 1
US-10-823-425-6 (1-32) x US-09-949-016-17149 (1-83349)
QY 7 LysIleGlyIleGlyAlaValLeuLysValLeuThrThrGlyLeuPro--- 25
Db 57780 AGAGTTGGGTGGGGGGGTGTTGAAGATCTTGAAGGTCCTTAAGCCTGGCCCTCTCCCT 57839
QY 26 -----AlaLeuLysLeuThrLeu 31
Db 57840 CACCACGACATCTCCATGACTCTT 57863

RESULT 13
US-09-949-016-175049/c
Sequence 175049, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 175049
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-175049

Alignment Scores:
Pred. No.: 2.75 Length: 601
Score: 56.00 Matches: 12
Percent Similarity: 80.95% Conservative: 5
Best Local Similarity: 57.14% Mismatches: 4
Query Match: 35.67% Indels: 0
DB: Gaps: 0

US-10-823-425-6 (1-32) x US-09-949-016-175049 (1-601)

QY 12 AlaValLeuLysValLeuLysValLeuThrThrGlyLeuProAlaLeuThrLeu 31
Db 438 GCGTGTCTCTGTCTGACAGAGCGCTGACACAGGAATACACGCCCTCTCCCTGTCTCTG 379

QY 32 Lys 32
Db 378 CGC 376

RESULT 14
US-09-949-016-175050/c
Sequence 175050, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012

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; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 175050
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-175050

Alignment Scores:
Pred. No.:      2.75      Length:      601
Score:          56.00     Matches:      12
Percent Similarity: 80.95% Conservative: 5
Best Local Similarity: 57.14% Mismatches: 4
Query Match:    35.67%   Indels:      0
DB:             3       Gaps:        0

US-10-823-425-6 (1-32) x US-09-949-016-175050 (1-601)

QY      12 AlaValLeuLysValLeuThrThrGlyLeuProAlaLeuLysLeuThrLeu 31
Db      475 GCGTGTCTCTGTCAGAGAGCCCTGAGCACAGGATACAGCCCTTCCCTGTCTCTG 416

QY      32 Lys 32
Db      415 CGC 413

RESULT 15
US-10-152-886-24
; Sequence 24, Application US/10152886
; Patent No. 6912470
; GENERAL INFORMATION:
; APPLICANT: ECOPIA BIOSCIENCES INC.
; APPLICANT: Farnet, Chris
; APPLICANT: Staiffa, Alfredo
; APPLICANT: Zazopoulos, Emmanuel
; TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF ENEDIYNE RING
; FILE REFERENCE: 3011-3US
; CURRENT APPLICATION NUMBER: US/10/152,886
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 5871
; TYPE: DNA
; ORGANISM: Streptomyces ghanaensis
US-10-152-886-24

Alignment Scores:
Pred. No.:      52.8      Length:      5871
Score:          56.00     Matches:      13
Percent Similarity: 65.38% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 9
Query Match:    35.67%   Indels:      0
DB:             3       Gaps:        0

US-10-823-425-6 (1-32) x US-10-152-886-24 (1-5871)

QY      4 LeuPheLysIleGlyIleGlyAlaValLeuLysValLeuThrThrGly 23
Db      2476 CTGTTGTGAGTGGAGCCGCGGTGCTCAGCGGCTCGCCGGGCCACACCGGT 2535

QY      24 LeuProAlaLeuLysLeu 29
Db      2536 GTCCCGCGCGTCGCCCTG 2553

Search completed: January 15, 2006, 22:29:42
Job time : 164 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 19:30:41 ; Search time 816 Seconds
(without alignments)
324.289 Million cell updates/sec

Title: US-10-823-425-6
Perfect score: 157
Sequence: 1 KWLKPKIGIGAVLKVLTGLPALKLTIX 32

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
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-THR MAX=100 -THR MIN=0 -ALIGN=0 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10823425 @CNCN 1.1 1549 @runat_13012006_095449_27988 -NCPU=6 -ICPU=3
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-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123.5	78.7	105	7	US-10-421-635-3 Sequence 3, Appli
2	120.5	76.8	87	7	US-10-421-635-1 Sequence 1, Appli
3	64	40.8	1245	7	US-10-320-797-2192 Sequence 2192, Ap
C 4	62	39.5	700	8	US-10-425-115-166548 Sequence 166548,
C 5	60	38.2	1770	7	US-10-282-122A-24588 Sequence 24588, A
C 6	58	36.9	569	4	US-09-925-065A-368393 Sequence 368393,
7	58	36.9	1447	7	US-10-425-114-36096 Sequence 36096, A

C 8	58	36.9	3250	7	US-10-425-114-31051 Sequence 31051, A
C 9	58	36.9	3300	8	US-10-425-115-108675 Sequence 108675,
10	57	36.3	2623	7	US-10-425-114-34026 Sequence 34026, A
11	57	36.3	2672	8	US-10-425-115-32143 Sequence 32143, A
12	57	36.3	4710	7	US-10-398-221-685 Sequence 685, App
13	57	36.3	4710	7	US-10-398-221-2079 Sequence 2079, Ap
14	57	36.3	81905	7	US-10-398-221-2057 Sequence 2057, Ap
15	57	36.3	82689	7	US-10-398-221-11 Sequence 11, Appl
16	56.5	36.0	637	5	US-10-027-632-206183 Sequence 206183,
17	56.5	36.0	637	5	US-10-027-632-206183 Sequence 206183,
18	56	35.7	277	3	US-09-987-899-4536 Sequence 4536, Ap
19	56	35.7	478	7	US-10-437-963-101232 Sequence 101232,
20	56	35.7	2766	6	US-10-108-260A-1119 Sequence 1119, Ap
21	56	35.7	5871	5	US-10-152-886-24 Sequence 24, Appl
22	56	35.7	5871	10	US-11-053-576-24 Sequence 24, Appl
23	56	35.7	5871	10	US-11-053-576-24 Sequence 24, Appl
C 24	55.5	35.4	22005	6	US-10-292-198-2 Sequence 2, Appli
25	55.5	35.4	1356	9	US-10-501-282-1563 Sequence 1563, Ap
26	55.5	35.4	1754382	9	US-10-501-282-6651 Sequence 6651, Ap
C 27	55	35.0	620	5	US-10-027-632-103202 Sequence 103202,
C 28	55	35.0	620	6	US-10-027-632-103202 Sequence 103202,
C 29	55	35.0	761	5	US-10-027-632-28686 Sequence 28686, A
C 30	55	35.0	761	6	US-10-027-632-28686 Sequence 28686, A
C 31	55	35.0	788	4	US-09-925-065A-18648 Sequence 18648, A
C 32	55	35.0	1132	4	US-09-925-065A-706593 Sequence 706593,
33	54.5	34.7	216	8	US-10-425-115-59804 Sequence 59804, A
34	54	34.4	452	8	US-10-425-115-13628 Sequence 13628, A
C 35	54	34.4	477	3	US-09-881-752A-335 Sequence 335, App
C 36	54	34.4	722	5	US-10-027-632-161756 Sequence 161756,
C 37	54	34.4	722	6	US-10-027-632-161756 Sequence 161756,
38	54	34.4	1377	9	US-10-845-366-21 Sequence 21, Appl
39	54	34.4	109565	7	US-10-322-281-27 Sequence 27, Appl
40	53.5	34.1	486	3	US-09-855-604-383 Sequence 383, App
41	53.5	34.1	486	3	US-09-855-604-383 Sequence 383, App
42	53.5	34.1	498	3	US-09-855-604-385 Sequence 385, App
43	53.5	34.1	498	3	US-09-855-604-385 Sequence 385, App
C 44	53.5	34.1	603	4	US-09-925-065A-921342 Sequence 921342,
C 45	53.5	34.1	603	4	US-09-925-065A-946494 Sequence 946494,

ALIGNMENTS

RESULT 1
US-10-421-635-3
; Sequence 3, Application US/10421635
; Publication NO. US20040064847A1
; GENERAL INFORMATION:
; APPLICANT: Misra, Santosh et al.
; TITLE OF INVENTION: Transgenic Plants Exhibiting Resistance to a Spectrum of Pathogens
; FILE REFERENCE: 55682
; CURRENT APPLICATION NUMBER: US/10/421,635
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: US/09/616,110
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/165,249
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
; OTHER INFORMATION: sequence encoding ECEMA
US-10-421-635-3

Alignment Scores:
Pred. No.: 6.88e-12 Length: 105
Score: 123.50 Matches: 27
Percent Similarity: 90.00% Conservativeness: 0
Best Local Similarity: 90.00% Mismatches: 0


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; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 24588
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Listeria monocytogenes
US-10-282-122A-24588

Alignment Scores:
Pred. No.: 20.6 Length: 1770
Score: 60.00 Matches: 12
Percent Similarity: 62.96% Conservative: 5
Best Local Similarity: 44.44% Mismatches: 10
Query Match: 38.22% Indels: 0
DB: 7 Gaps: 0

US-10-823-425-6 (1-32) x US-10-282-122A-24588 (1-1770)

Qy 5 PheLysLysLeuGlyLeuGlyAlaValLeuLysValLeuLysValLeuThrGlyLeu 24
Db 503 TTTCAAAAGAGTTAAATTTGGAGTTATTAAATTTGTCAAGCACTATTATCTAGTTTA 444
Qy 25 PheLysLysLeuThrLeu 31
Db 443 CCGGAACCTTAAGTTAAGTTG 423

RESULT 6
US-09-925-065A-368393/c
; Sequence 368393, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
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; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 368393
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-368393

Alignment Scores:
Pred. No.: 10.2 Length: 569
Score: 58.00 Matches: 12
Percent Similarity: 67.86% Conservative: 7
Best Local Similarity: 42.86% Mismatches: 9
Query Match: 36.94% Indels: 0
DB: 4 Gaps: 0

US-10-823-425-6 (1-32) x US-09-925-065A-368393 (1-569)

Qy 4 LeuPheLysLysLeuGlyLeuGlyAlaValLeuLysValLeuLysValLeuThrGly 23
Db 148 ATGTTCAACCAAGTCACATAGGGCTGTGTTTCAGAGCTCTTATCTCACTTCAGGG 89
Qy 24 LeuProAlaLeuLysLeuThrLeu 31
Db 88 CTCCTCGCTGATGGAGCTGCCACTA 65

RESULT 7
US-10-425-114-36096
; Sequence 36096, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36096
; LENGTH: 1447
; TYPE: DNA
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROTEOSINTE070F12_FLI
US-10-425-114-36096

Alignment Scores:
Pred. No.: 34.8 Length: 1447
Score: 58.00 Matches: 13
Percent Similarity: 64.52% Conservative: 7
Best Local Similarity: 41.94% Mismatches: 9
Query Match: 36.94% Indels: 2
DB: 7 Gaps: 1

US-10-823-425-6 (1-32) x US-10-425-114-36096 (1-1447)

Qy 2 TrpLysLeuPheLysLysLeuGlyLeuGlyAlaValLeuLysValLeuLysValLeuThr 21
Db 509 TGGAGCAGACTCAAGAAATTAGCCCTG-----TTGATCTTCTAGAAAGGTGTGACA 562
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Qy 22 ThrGlyLeuProAlaLeuLysLeuThrLeuLys 32
||||| ||| |:::|:::
Db 563 GTTTCACCTCCAAATCTTCATCGAGCTGAGA 595

RESULT 8

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US-10-425-114-31051
; Sequence 31051, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 31051
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73121B01_FLI
US-10-425-114-31051

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Alignment Scores:		
Pred. No.:	101	Length: 3250
Score:	58.00	Matches: 13
Percent Similarity:	64.52%	Conservative: 9
Best Local Similarity:	41.94%	Mismatches: 7
Query Match:	36.94%	Indels: 2
DB:	7	Gaps: 1

US-10-823-425-6 (1-32) x US-10-425-114-31051 (1-3250)

QY 2 TrpLysLeuPheLysLysIleGlyIleGlyAlaValLeuLysValLeuLysValLeuThr 21

QY 22 ThrGlyLeuProAlaLeuLysLeuThrLeuLys 32
 ||||| ||| |||::|:::
 Db 2064 GTTTCACCTTCCAATTCTTCCATTGAGCTGAGA 2098

RESULT 9

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US-10-425-115-108675/c
; Sequence 108675, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: Thomas J.
; APPLICANT: La Rosa, David K.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 108675
; LENGTH: 3300
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_30605C.1
US-10-425-115-108675

```

Alignment Scores:	
Pred. No.:	103
Score:	58.00
Length:	3300
Matches:	13

Percent Similarity:	64.52%	Conservative:	7
Best Local Similarity:	41.94%	Mismatches:	9
Query Match:	36.94%	Indels:	2
DB:	8	Gaps:	1

US-10-823-425-6 (1-32) x US-10-425-115-108675 (1-3300)

Qy	2	TripLysLeuPheLysIleGlyAlaValLeuLysValLeuLysValLeuThr	21
Db	1241	TGGAGCAGACTCAAGAATATGSCCTG-----TTGATCTTCTAGGAAGGTGTTCACA ::::: ::: : : :	11889

QY 22 ThrGlyLeuProAlaLeuLysLeuThrLeuLys 32
||||| ||| |::||:::
Dd 1187 GTTTCACCTCCAAATCTCCATTGAGCCTGAGA 1197

RESULT 10

```

US-10-425-114-34026
US-10-425-114-34026, Application US/10425114
; Sequence 34026, Application US/10425114
; Publication No. US2004003488A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Liu, Jingdong
;
; APPLICANT: Zhou, Yihua
;
; APPLICANT: Kovalic, David K.
;
; APPLICANT: Screen, Steven E
;
; APPLICANT: Tabaska, Jack E
;
; APPLICANT: Cao, Yongwei
;
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;
; FILE REFERENCE: 38-21(53313)B
;
; CURRENT APPLICATION NUMBER: US/10/425,114
;
; CURRENT FILING DATE: 2003-04-28
;
; NUMBER OF SEQ ID NOS: 73128
;
; SEQ ID NO 34026
;
; LENGTH: 2623
;
; TYPE: DNA
;
; ORGANISM: Zea mays
;
; FEATURE:
;
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17209B01_FLI
;
; US-10-425-114-34026

```

Alignment Scores:			
Pred. No.:	113	Length:	2623
Score:	57.00	Matches:	12
Percent Similarity:	88.24%	Conservative:	3
Best Local Similarity:	70.59%	Mismatches:	20
Query Match:	36.31%	Indels:	0
Da:	7	Gaps:	0

US-10-823-425-6 (1-32) x US-10-425-114-34026 (1-2623)

Qy

4 LeuPheLysLysIleGlyIleGlyAlaValLeuLysValLeuLysValLeu 20
||||| ::|||:::||| ::|||::|||::|||::|||::|||::|||::|||

Dh

139 CTGTCTTTGGCAAAATCGAATTGGAGTGGAGGCACCATGAAGTTTTTGAGGTTTTG 189

DEC 11 1961

```

RESULT 11
US-10-425-115-32143
; Sequence 32143, Application US/10425115
; Publication NO. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 39-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 32143
; LENGTH: 2672
; TYPE: DNA
; ORGANISM: Zea mays

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; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_129328C.1
US-10-425-115-32143

Alignment Scores:
Pred. No.: 115 Length: 2672
Score: 57.00 Matches: 12
Percent Similarity: 88.24% Conservatives: 3
Best Local Similarity: 70.59% Mismatches: 2
Query Match: 36.31% Indels: 0
DB: 8 Gaps: 0

US-10-823-425-6 (1-32) x US-10-425-115-32143 (1-2672)
QY 4 LeuPheLysLeuGlyAlaValLeuLysValLeu 20
Db 139 CTGTTTGGCAATGGAATGGGAGCGACAAATGAAAGTTTGAAGGTTTG 189

RESULT 12
US-10-398-221-685
; Sequence 685, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 685
; LENGTH: 4710
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-685

Alignment Scores:
Pred. No.: 243 Length: 4710
Score: 57.00 Matches: 12
Percent Similarity: 71.43% Conservatives: 8
Best Local Similarity: 42.86% Mismatches: 8
Query Match: 36.31% Indels: 0
DB: 7 Gaps: 0

US-10-823-425-6 (1-32) x US-10-398-221-685 (1-4710)
QY 3 LysLeuPheLysLeuGlyAlaValLeuLysValLeuThr 22
Db 2087 AAATTTGTTCAAAAAGTTGGAGATCGTAATAATCTTGAGAAATGGTCAAGATGTTGCTA 2146

RESULT 13
US-10-398-221-2079
; Sequence 2079, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 685
; LENGTH: 4710
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-2079

Alignment Scores:
Pred. No.: 243 Length: 4710
Score: 57.00 Matches: 12
Percent Similarity: 71.43% Conservatives: 8
Best Local Similarity: 42.86% Mismatches: 8
Query Match: 36.31% Indels: 0
DB: 7 Gaps: 0

US-10-823-425-6 (1-32) x US-10-398-221-2079 (1-4710)
QY 3 LysLeuPheLysLeuGlyAlaValLeuLysValLeuThr 22
Db 2087 AAATTTGTTCAAAAAGTTGGAGATCGTAATAATCTTGAGAAATGGTCAAGATGTTGCTA 2146

RESULT 14
US-10-398-221-2057/c
; Sequence 2057, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2057
; LENGTH: 81905
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-2057

Alignment Scores:
Pred. No.: 1,046+04 Length: 81905
Score: 57.00 Matches: 12
Percent Similarity: 71.43% Conservatives: 8
Best Local Similarity: 42.86% Mismatches: 8
Query Match: 36.31% Indels: 0
DB: 7 Gaps: 0

US-10-823-425-6 (1-32) x US-10-398-221-2057 (1-81905)
QY 3 LysLeuPheLysLeuGlyAlaValLeuLysValLeuThr 22
Db 18104 AAATTTGTTCAAAAAGTTGGAGATCGTAATAATCTTGAGAAATGGTCAAGATGTTGCTA 18045

RESULT 15
US-10-398-221-11/c
; Sequence 11, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
```

APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 82689
TYPE: DNA
ORGANISM: Listeria innocua
US-10-398-221-11

Alignment Scores:
Pred. No.: 1.05e+04 Length: 82689
Score: 57.00 Matches: 12
Percent Similarity: 71.43% Conservative: 8
Best Local Similarity: 42.86% Mismatches: 8
Query Match: 36.31% Indels: 0
DB: 7 Gaps: 0

US-10-823-425-6 (1-32) x US-10-398-221-11 (1-82689)
QY 3 LysLeuPheLysLysIleGlyIleGlyAlaValLeuLysValLeuThrThr 22
Db 4819 AAATTGTTCAAAAAGTTGGAGATCGTAATATCTTGAGAAATTGGTCCAAAGATGTTGCTA 4760
QY 23 GlyLeuProAlaLeuLysLeuThr 30
Db 4759 AAATTGCCGAGCGTCAAAATTAAT 4736

Search completed: January 15, 2006, 22:48:32
Job time : 843 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2006, 20:34:03 ; Search time 393 Seconds
(without alignments)
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Title: US-10-823-425-6
Perfect score: 157
Sequence: 1 KWKLKKIGIGAVLKVLTGLPALKJTLK 32

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications NA_New:

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- 4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq*
- 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq*
- 6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq*
- 7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq*
- 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3*
- 10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	53.5	34.1	33737	US-10-276-233A-7	Sequence 7, Appli
C 2	53.5	34.1	175100	US-11-121-086-21	Sequence 21, Appl
C 3	53	33.8	201	US-11-124-368A-4602	Sequence 4602, Ap
C 4	53	33.8	2221	US-10-750-185-28230	Sequence 28230, A
C 5	53	33.8	2221	US-10-750-623-28230	Sequence 28230, A
C 6	52.5	33.4	1608	US-11-114-906-15	Sequence 15, Appl
C 7	52.5	33.4	1647	US-11-114-906-13	Sequence 13, Appl
C 8	52.5	33.4	1947	US-11-114-906-11	Sequence 11, Appl

9	52.5	33.4	1965	7	US-11-114-906-9	Sequence 9, Appli
10	52.5	33.4	2256	7	US-11-114-906-7	Sequence 7, Appli
11	52.5	33.4	2295	7	US-11-114-906-5	Sequence 5, Appli
12	52.5	33.4	2331	7	US-11-114-906-23	Sequence 23, Appl
13	52.5	33.4	2370	7	US-11-114-906-21	Sequence 21, Appl
14	52.5	33.4	2517	7	US-11-114-906-39	Sequence 39, Appl
15	52.5	33.4	2556	7	US-11-114-906-37	Sequence 37, Appl
16	52.5	33.4	2592	7	US-11-114-906-31	Sequence 31, Appl
17	52.5	33.4	2595	7	US-11-114-906-3	Sequence 3, Appli
18	52.5	33.4	2613	7	US-11-114-906-1	Sequence 1, Appli
19	52.5	33.4	2631	7	US-11-114-906-29	Sequence 29, Appl
20	52.5	33.4	2670	7	US-11-114-906-19	Sequence 19, Appl
21	52.5	33.4	2688	7	US-11-114-906-17	Sequence 17, Appl
22	52.5	33.4	2856	7	US-11-114-906-35	Sequence 35, Appl
23	52.5	33.4	2874	7	US-11-114-906-33	Sequence 33, Appl
24	52.5	33.4	2931	7	US-11-114-906-27	Sequence 27, Appl
25	52.5	33.4	2949	7	US-11-114-906-25	Sequence 25, Appl
26	52	33.1	1400	7	US-11-136-527-4710	Sequence 4710, Ap
27	52	33.1	1770	6	US-10-821-234-642	Sequence 642, App
C 28	52	33.1	2357	6	US-10-947-249-99	Sequence 99, Appl
C 29	52	33.1	2947	7	US-11-136-527-144	Sequence 144, App
30	52	33.1	3012	7	US-11-136-527-614	Sequence 614, App
C 31	51.5	32.8	4517	6	US-10-750-185-30213	Sequence 30213, A
C 32	51.5	32.8	4517	6	US-10-750-623-30213	Sequence 30213, A
C 33	51	32.5	201	6	US-10-995-561-37030	Sequence 37030, A
C 34	51	32.5	201	6	US-10-995-561-78619	Sequence 78619, A
C 35	51	32.5	3300	6	US-10-873-528-219	Sequence 219, App
C 36	51	32.5	93112	6	US-10-995-561-13234	Sequence 13234, A
C 37	51	32.5	170508	7	US-11-112-908-62	Sequence 62, Appl
C 38	51	32.5	173115	7	US-11-112-908-65	Sequence 65, Appl
C 39	51	32.5	340000	7	US-11-102-978-3	Sequence 3, Appli
40	50	31.8	524	7	US-11-128-061-2211	Sequence 2211, App
41	50	31.8	524	7	US-11-128-061-5853	Sequence 5853, Ap
C 42	50	31.8	965	6	US-10-750-185-62417	Sequence 62417, A
C 43	50	31.8	965	6	US-10-750-623-62417	Sequence 62417, A
44	50	31.8	1556	6	US-10-750-185-36358	Sequence 36358, A
45	50	31.8	1556	6	US-10-750-623-36358	Sequence 36358, A

ALIGNMENTS

RESULT 1
US-10-276-233A-7/c
; Sequence 7, Application US/10276233A
; Publication No. US20050260572A1
; GENERAL INFORMATION:
; APPLICANT: DNA Chip Research Inc.
; APPLICANT: Hitachi Software Engineering Co., Ltd. condition
; TITLE OF INVENTION: A method of predicting cancer condition
; FILE REFERENCE: PH-1533-PCT
; CURRENT APPLICATION NUMBER: US/10/276,233A
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: JP 2001-73063
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: JP 2001-108503
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: JP 2001-234807
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 33737
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-233A-7

Alignment Scores:
Pred. No.: 7.49e+03
Score: 53.50
Percent Similarity: 69.57%
Best Local Similarity: 47.83%
Query Match: 34.08%
DB: 6
Length: 33737
Matches: 11
Conservative: 5
Mismatches: 6
Indels: 1
Gaps: 1

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US-10-823-425-6 (1-32) x US-10-276-233A-7 (1-33737)
QY 2 TrpLysLeuPheLysIleGlyAlaValLeuLysValLeuLysValLeu 20
Db 26449 TGGGACCTCTTTGAGAAGTTGGGAATGGTGGGAGGTCCTTGATGCCCCACATCCTC 26390
QY 21 ThrThrGly 23
Db 26389 AGCACTGGA 26381

RESULT 2
US-11-121-086-21/c
; Sequence 21, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, KIRSTEN V.
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 175100
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-21

Alignment Scores:
Pred. No.: 7,36e+04 Length: 175100
Score: 53.50 Matches: 11
Percent Similarity: 69.57% Conservative: 5
Best Local Similarity: 47.83% Mismatches: 6
Query Match: 34.08% Indels: 1
DB: 7 Gaps: 1

US-10-823-425-6 (1-32) x US-11-121-086-21 (1-175100)
QY 2 TrpLysLeuPheLysIleGlyAlaValLeuLysValLeuLysValLeu 20
Db 79917 TGGGACCTCTTTGAGAAGTTGGGAATGGTGGGAGGTCCTTGATGCCCCACATCCTC 79850
QY 21 ThrThrGly 23
Db 79857 AGCACTGGA 79849

RESULT 3
US-11-124-368A-4602
; Sequence 4602, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4602
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-11-124-368A-4602
Alignment Scores:
Pred. No.: 7,51 Length: 201
Score: 53.00 Matches: 13
Percent Similarity: 69.23% Conservative: 5
Best Local Similarity: 50.00% Mismatches: 4
Query Match: 33.76% Indels: 4
DB: 7 Gaps: 1

US-10-823-425-6 (1-32) x US-11-124-368A-4602 (1-201)
QY 2 TrpLysLeuPheLysIleGlyAlaValLeuLysValLeuLysValLeuThr 21
Db 70 TTTGAGCTCTTTAAAAAGATAGGACTGGCCRGATGCTG-----TGGCTCAG 117
QY 22 ThrGlyLeuProAlaLeu 27
Db 118 CCTGTAATCCAGCACCTT 135

RESULT 4
US-10-750-185-28230/c
; Sequence 28230, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28230
; LENGTH: 2221
; TYPE: DNA
; ORGANISM: Bovine 19866880140920
US-10-750-185-28230

Alignment Scores:
Pred. No.: 210 Length: 2221
Score: 53.00 Matches: 14
Percent Similarity: 64.29% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 8
Query Match: 33.76% Indels: 2
DB: 6 Gaps: 1

US-10-823-425-6 (1-32) x US-10-750-185-28230 (1-2221)
QY 4 LeuPheLysIleGlyAlaValLeuLysValLeuLysValLeuLysValLeuThr 21
Db 870 TTGGTTCTCCAACTAGGAGCTGCTGCTCCCTCGCAGTGAAGCATGGGTTTTTAAC 811
QY 22 ThrGlyLeuProAlaLeuLysLeu 29
Db 810 ACTGGATTCCAGAGATATCCCTT 787

RESULT 5
US-10-750-623-28230/c
; Sequence 28230, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
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; TITLE OF INVENTION: NOVEL HUMAN KINASES AND POLYNUCLEOTIDES ENCODING THE SAME
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/11/1114,906
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: US/10/413,437
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 2370
; TYPE: DNA
; ORGANISM: homo sapiens
US-11-114-906-21

Alignment Scores:
Pred. No.:      282           Length:    2370
Score:          52.50        Matches:     12
Percent Similarity: 59.38%   Conservative:  7
Best Local Similarity: 37.50% Mismatches:    10
Query Match:     33.44%     Indels:       3
DB:              7         Gaps:         1

US-10-823-425-6 (1-32) x US-11-114-906-21 (1-2370)

QY      1  LysTpLysLeuPheLysLysLysLle-----GlyIlegLyAlaValLeuLysValLeu 17
Db      97  CGCTGGAGGTCTCGAAAGAATCGGGGGCGGGCGCTTTTGTGTGAGATTACGAGGCCCATG 156

QY      18  LysValLeuThrThrGlyLeuProAlaLeuLysLeu 29
Db     157  GACCTGTCGACCAGGGAGGAATGTGGCCCTCAAGGTG 192

RESULT 14
US-11-114-906-39
; Sequence 39, Application US/11114906
; Publication No. US20050266452A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: NOVEL HUMAN KINASES AND POLYNUCLEOTIDES ENCODING THE SAME
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/11/1114,906
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: US/10/413,437
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 2517
; TYPE: DNA
; ORGANISM: homo sapiens
US-11-114-906-39

Alignment Scores:
Pred. No.:      307           Length:    2517
Score:          52.50        Matches:     12
Percent Similarity: 59.38%   Conservative:  7
Best Local Similarity: 37.50% Mismatches:    10
Query Match:     33.44%     Indels:       3
DB:              7         Gaps:         1

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US-10-823-425-6 (1-32) x US-11-114-906-39 (1-2517)

Qy	1	LysTrpLysLeuPheLysIle-----GlyIleGlyAlaValLeuLysValLeu	17
Db	58	CGTGGAAGTCTCTGAAAGAATCGGGGGCGGGCGCTTTGTGAGATCTACGAGGCCATG	117
Qy	18	LysValLeuThrThrGlyLeuProAlaLeuLysLeu	29
Db	118	GACCTCTCAACAGGGAGAAATGTGGCCCTCAAGGTG	153

RESULT 15

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US-11-114-906-37
; Sequence 37, Application US/11114906
; Publication NO. US20050266452A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fiddle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/11/114,906
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: US/10/413,437
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 2556
; TYPE: DNA
; ORGANISM: homo sapiens
US-11-114-906-37

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Alignment Scores:		
Pred. No.:	313	Length: 2556
Score:	52.50	Matches: 12
Percent Similarity:	59.33%	Conservative: 7
Best Local Similarity:	37.50%	Mismatches: 10
Query Match:	33.44%	Indels: 3
DB:	7	Gaps: 1

US-10-823-425-6 (1-32) X US-11-114-906-37 (1-2556)

QY 1 LysTrpLysLeuPheLysGlySyle-----GlyTleGlyAlaValLeuLysValLeu 17
DB CGCTCGAAGGTTCCTGAATAAGATCGGGGCGGGGGCTTTTGAGATCTACGAGGCCATG 156
QY 18 LysValLeuThrThrGlyLeuProAlaLeuLysLeu 29
DB GACCTGCTGCACGAGGAGAATCTGGCCCTCAAGGT 192

Search completed: January 15, 2006. 22:55:15

search completed: Jan
Job time : 413 sec